

## 6800 chip human RA PBMC

name	qualifier	GeneSpring qualifier	Patients called "P">4	#"P" (RA)	Avg Freq RA	Normals called "P">6 (Normal)	#"P" (RA)	Avg Freq Normals	Ratio	Fold Change	Symbol	Chromosome	Description	function
MR110000	D64154_at	D64154	fail	4	PASS	13	4	9.77	Normal	Normal	RAC2	22q12-q13.2	Mr 110,000 antigen	ras-related C3 botulinum toxin
RAC2	M64595_at	M64595	fail	3	PASS	13	3	19.85	Normal	Normal			substrate 2 (rho family, small GTP binding protein Rac2)	substrate 2 (rho family, small GTP binding protein Rac2)
J03263_s_at	J03263_s_at	J03263	fail	3	PASS	13	3	9.23	Normal	Normal	LAMP1		membrane glycoprotein	membrane glycoprotein
TBXAS1	M80647_at	M80647	fail	4	PASS	12	4	17.42	Normal	Normal	TBXAS1	7q34-q35	thromboxane A synthase 1 (platelet, cytochrome P450, subfamily V)	thromboxane A synthase 1 (platelet, cytochrome P450, subfamily V)
ALDR1	J04794_at	J04794	fail	4	PASS	12	4	14.42	Normal	Normal	ALDR1		hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit
HADHA	D16480_at	D16480	fail	2	PASS	12	2	16.33	Normal	Normal	HADHA	2p23	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit
M13929_s_at	M13929_s_at	M13929	fail	1	PASS	12	1	9.33	Normal	Normal	MYC		c-myc-P64 protein	ORF 114; putative
HLK1	U40462_at	U40462	fail	1	PASS	12	1	6.42	Normal	Normal	hlk-1		Ikaros/LyF-1 homolog	similar to mouse LyF-1, encoded by GenBank Accession Number S74708; similar to mouse Ikaros DNA-binding protein, Swiss-Prot Accession Number Q03267
MANA2	D63998_at	D63998	fail	1	PASS	12	1	5.25	Normal	Normal	MANA2	5	mannosidase, alpha type II	mannosidase, alpha type II
ITBA2	X92896_at	X92896	fail	0	PASS	12	0	6.42	Normal	Normal	ITBA2		protein phosphatase inhibitor 2	
PPP1R2	U68111_at	U68111	fail	0	PASS	12	0	5.17	Normal	Normal	PPP1R2		FYN-binding protein (FYN-120/130)	FYN-binding protein (FYN-120/130)
LCP2	U93049_at	U93049	fail	3	PASS	11	3	11.82	Normal	Normal	FYB		RNA polymerase II	
PCNA	J05614_at	J05614	fail	3	PASS	11	3	11.73	Normal	Normal			rab8 small GTP binding	
POLR2B	L37127_at	L37127	fail	2	PASS	11	2	13.27	Normal	Normal			dihydropyrimidine dehydrogenase	dihydropyrimidine dehydrogenase
DG	HG1872-HT	HG1872-HT	fail	2	PASS	11	2	10.55	Normal	Normal	rab8		CALM	
MEL	X56741_at	X56741	fail	2	PASS	11	2	7.82	Normal	Normal	DPYD	1p22	transducin-like enhancer protein	transducin-like enhancer of split 4, homolog of Drosophila E(spl)
U09178_s_at	U09178_s_at	U09178	fail	2	PASS	11	2	6.91	Normal	Normal			heat shock 70kD protein 4	heat shock 70kD protein 4
CALM	U45976_at	U45976	fail	2	PASS	11	2	6.91	Normal	Normal	CALM		nucleolar protein p40	cell proliferation-associated protein
TLE4	M99439_at	M99439	fail	2	PASS	11	2	5.73	Normal	Normal	TLE4		T-complex protein 1, Beta subunit (TCP-1-BETA)	
HSPA4	L12723_at	L12723	fail	2	PASS	11	2	5.45	Normal	Normal	HSPA4	5q31.1-q31.2	FKBP-rapamycin associated protein	FK506 binding protein 12-rapamycin associated protein 1
NUCP40	U86602_at	U86602	fail	2	PASS	11	2	5.09	Normal	Normal			eukaryotic translation initiation factor 2, subunit 3 (gamma, 52kD)	eukaryotic translation initiation factor 2, subunit 3 (gamma, 52kD)
E_CIT987SK	U91327_at	U91327	fail	1	PASS	11	1	5.82	Normal	Normal	99D8.1		E46-like contains exons 2-9 continues in Z84478	E46-like contains exons 2-9 continues in Z84478
FRAP	L34075_at	L34075	fail	1	PASS	11	1	5.73	Normal	Normal	FRAP1	1p36.2	ubiquitin carboxyl-terminal hydrolase	ubiquitin carboxyl-terminal hydrolase
EIF2G	L19161_at	L19161	fail	1	PASS	11	1	5.64	Normal	Normal	EIF2S3	Xp22.2-p22.1		
P_E46	Z93784_at	Z93784	fail	1	PASS	11	1	5.36	Normal	Normal	dJ398C22.1			
UCHL3	M30496_at	M30496	fail	1	PASS	11	1	4.27	Normal	Normal				

RPA1	M63488_at	M63488	fail	0		PASS	11	0	7.45	Normal	Normal	RPA1	17	replication protein A1 (70kD)	replication protein A1 (70kD)
RUNF	HG511-HT3	HG511-HT3	fail	0		PASS	11	0	5.36	Normal	Normal	HLA-DQA1	6p21.3	major histocompatibility complex, class II, DQ alpha 1	major histocompatibility complex, class II, DQ alpha 1
M26041_s_at	M26041_s_at	M26041	fail	3		PASS	10	3	20.70	Normal	Normal	SIP	16	site-1 protease (ubiquitin-like, sterol-regulated, cleaves sterol regulatory element binding proteins)	site-1 protease (ubiquitin-like, sterol-regulated, cleaves sterol regulatory element binding proteins)
K91_PCSK	D42053_at	D42053	fail	2		PASS	10	2	6.70	Normal	Normal	KVLQT1		voltage gated potassium channel, class D, KVLQT1 (Krabbe disease)	galactosylceramidase (Krabbe disease)
KCNQ1	U40990_at	U40990	fail	2		PASS	10	2	6.70	Normal	Normal	GALC	14q31	galactosylceramidase (Krabbe disease)	galactosylceramidase (Krabbe disease)
GALC	L23116_at	L23116	fail	2		PASS	10	2	5.40	Normal	Normal	KPNB3		karyopherin (importin) beta 3	karyopherin (importin) beta 3
KPNB3	U72761_at	U72761	fail	2		PASS	10	2	5.40	Normal	Normal	DR1	1p22.1	down-regulator of transcription 1, TBP-binding (negative cofactor 2)	down-regulator of transcription 1, TBP-binding (negative cofactor 2)
DR1	M97388_at	M97388	fail	2		PASS	10	2	5.30	Normal	Normal	RFC4	3q27	replication factor C (activator 1) 4 (37kD)	replication factor C (activator 1) 4 (37kD)
RFC4	M87339_at	M87339	fail	2		PASS	10	2	5.20	Normal	Normal	MAN2A2	15q25	alpha mannosidase II isozyme	mannosidase, alpha, class 2A, member 2
BIOM	AFFX-BioB-1	AFFX-BioB-1	fail	1		PASS	10	1	7.20	Normal	Normal	CAMK2G	10q22	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma
UBE2D1	HG3344-HT3	HG3344-HT3	fail	1		PASS	10	1	6.50	Normal	Normal	POH1		26S proteasome-associated pad1 homolog	human homolog of fission yeast pad1
MANA2	L28821_at	L28821	fail	1		PASS	10	1	6.30	Normal	Normal			esterase D	
CAMKA2	U81554_at	U81554	fail	1		PASS	10	1	5.50	Normal	Normal			inhibitor of apoptosis protein 1	HIAP-1
HG2797-HT3	HG2797-HT3	HG2797-HT3	fail	1		PASS	10	1	5.20	Normal	Normal			ribosomal protein S4, Y-linked	ribosomal protein S4, Y-linked
POH1	U86782_at	U86782	fail	1		PASS	10	1	5.00	Normal	Normal			far upstream element binding protein	putative far upstream element binding protein
GZMM	HG3104-HT3	HG3104-HT3	fail	0		PASS	10	0	16.20	Normal	Normal			CD27 antigen	tumor necrosis factor receptor superfamily, member 7
BAP	U72512_at	U72512	fail	3		PASS	9	3	13.56	Normal	Normal			cysteine-rich fibroblast growth factor receptor	
ESD	D28416_at	D28416	fail	3		PASS	9	3	10.89	Normal	Normal			protein tyrosine phosphatase, receptor type, alpha polypeptide	protein tyrosine phosphatase, receptor type, alpha polypeptide
KO1160_s_at	KO1160_s_at	KO1160	fail	3		PASS	9	3	10.00	Normal	Normal			SMC (mouse) homolog, Y chromosome	SMC (mouse) homolog, Y chromosome
U45878_s_at	U45878_s_at	U45878	fail	3		PASS	9	3	9.22	Normal	Normal			putative DNA dependent ATPase and helicase	XH2; XNP; alternately spliced product 1; translation starts in exon 9
RPS4Y	M58459_at	M58459	fail	2		PASS	9	2	44.67	Normal	Normal			carboxyl reductase 1	carboxyl reductase 1
LTR	M92449_at	M92449	fail	2		PASS	9	2	9.89	Normal	Normal			heat shock 27kD protein 1	heat shock 27kD protein 1
FBP1	U05040_at	U05040	fail	2		PASS	9	2	7.67	Normal	Normal				
CD27	M63928_at	M63928	fail	2		PASS	9	2	7.44	Normal	Normal				
FGFR1	U28811_at	U28811	fail	2		PASS	9	2	6.11	Normal	Normal				
PTPRA	M34668_at	M34668	fail	2		PASS	9	2	5.67	Normal	Normal				
U52191_s_at	U52191_s_at	U52191	fail	2		PASS	9	2	5.56	Normal	Normal				
U72935_cds3	U72935_cds3	U72935	fail	2		PASS	9	2	5.22	Normal	Normal				
CBR	J04056_at	J04056	fail	2		PASS	9	2	4.89	Normal	Normal				
HSPB1	Z23090_at	Z23090	fail	1		PASS	9	1	12.56	Normal	Normal				
STAT1Mb	AFEX-HUM1	AFEX-HUM1	fail	1		PASS	9	1	7.00	Normal	Normal				
K129_RP1	D50919_at	D50919	fail	1		PASS	9	1	4.89	Normal	Normal				

CDK7	L20320_at	L20320	fail	1		PASS	9	1	4.89	Normal	Normal	CDK7	2p15-cen	cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase)	cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase)
FABP5	M94856_at	M94856	fail	1		PASS	9	1	4.78	Normal	Normal	FABP5		fatty acid binding protein 5 (psoriasis-associated)	fatty acid binding protein 5 (psoriasis-associated)
ICSBP1	M91196_at	M91196	fail	0		PASS	9	0	8.33	Normal	Normal	ICSBP1		interferon consensus sequence binding protein 1	interferon consensus sequence binding protein 1
NMT1	M86707_at	M86707	fail	0		PASS	9	0	7.33	Normal	Normal	NMT1		N-myristoyltransferase 1	N-myristoyltransferase 1
RAB4	M28211_at	M28211	fail	0		PASS	9	0	5.11	Normal	Normal	RAB4	1q42-q43	RAB4, member RAS oncogene family	RAB4, member RAS oncogene family
ERPRT	M27826_at	M27826	fail	2		PASS	8	2	10.63	Normal	Normal			neutral protease large subunit	XXX; putative
EV12A	M55267_at	M55267	fail	2		PASS	8	2	10.13	Normal	Normal	EV12A		EV12 protein	
H2BH_f	Z80780_f	Z80780	fail	1		PASS	8	1	9.88	Normal	Normal	H2BH/h		histone H2B	
TIP60	U74667_at	U74667	fail	0		PASS	8	0	7.25	Normal	Normal	TIP60		tat interactive protein	interacts with HIV1 Tat, similar to acetyltransferase; similar to yeast SAS2, SAS3 and human MOZ, encoded by GenBank Accession Numbers U14548, Z23261 and U47742, respectively; similar to sequence with GenBank Accession Number U40989
PHB	S85655_at	S85655	fail	0		PASS	8	0	6.63	Normal	Normal	PHB	17q21	prohibitin	prohibitin
EPHB4	U07695_at	U07695	fail	0		PASS	8	0	6.50	Normal	Normal	EPHB4	7	EPHB4	EPHB4
SNAP23	U55936_at	U55936	fail	0		PASS	8	0	6.00	Normal	Normal	SNAP23		synaptosomal-associated protein, 23kD	synaptosomal-associated protein, 23kD
D26155_s_at	D26155_s_at	D26155	fail	0		PASS	8	0	5.13	Normal	Normal	SMARCA2	9p24-p23	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2
PRP4H	U48736_at	U48736	fail	0		PASS	8	0	5.00	Normal	Normal	PRP4		serine/threonine-protein kinase PRP4 homolog	serine/threonine-protein kinase PRP4 homolog
IL16	HG270-HT2	HG270-HT	fail	0		PASS	8	0	4.75	Normal	Normal				
E18CPGE	HG3991-HT4	HG3991-H	fail	4		PASS	7	4	30.57	Normal	Normal				
RORET	U90547_at	U90547	fail	4		PASS	7	4	12.14	Normal	Normal	RoRet		Ro/SSA ribonucleoprotein homolog	
HMG1Y_ma	L17131_ma	L17131	fail	4		PASS	7	4	9.71	Normal	Normal	HMG1Y	6p	high-mobility group (nonhistone chromosomal) protein isoforms I and Y	high-mobility group (nonhistone chromosomal) protein isoforms I and Y
APFX-BioDr	APFX-BioDr	APFX-BioDr	fail	2		PASS	7	2	12.29	Normal	Normal				
TXBP181	U33822_at	U33822	fail	1		PASS	7	1	9.86	Normal	Normal	MAD1L1	7p22	MAD1 (mitotic arrest deficient, yeast, homolog)-like 1	MAD1 (mitotic arrest deficient, yeast, homolog)-like 1
NUCB	U31342_at	U31342	fail	0		PASS	7	0	6.14	Normal	Normal			nucleobindin	
DPH2L	U34880_at	U34880	fail	0		PASS	7	0	6.00	Normal	Normal	DPH2L1	17p13.3	diphtheria toxin resistance protein required for diphtheramide biosynthesis (Saccharomyces)-like 1	diphtheria toxin resistance protein required for diphtheramide biosynthesis (Saccharomyces)-like 1
TRAP1	U12595_at	U12595	fail	0		PASS	7	0	5.71	Normal	Normal	TRAP1		tumor necrosis factor type 1 receptor associated protein	TNF type 1 receptor associated protein
X60003_s_at	X60003_s_at	X60003	fail	0		PASS	7	0	5.43	Normal	Normal	delta CREB			
2OGCP_ma	X66114_ma	X66114	fail	0		PASS	7	0	5.43	Normal	Normal	SLC20A4	17p13.3	solute carrier family 20 (oxoglutarate carrier), member 4	solute carrier family 20 (oxoglutarate carrier), member 4
K196	D83780_at	D83780	fail	0		PASS	7	0	5.14	Normal	Normal	KIAA0196		KIAA0196 gene product	KIAA0196 gene product





EFNB3	U66406_at	U66406	PASS	5	7.40	fail	0	5		Disease	EFNB3	17p13.1-p11.2	ephrit-B3	ephrit-B3
M87789_s at	M87789_s at	M87789	PASS	8	118.00	PASS	9	8	19.56	6.03			IgG	Anti-hepatitis A; putative
OC16	U45285_at	U45285	PASS	9	31.44	PASS	10	9	7.30	4.31			specific 116-kDa vacuolar proton pump subunit	ATPase, H <sup>+</sup> transporting, 116kD
UBE1	M58028_at	M58028	PASS	9	46.44	PASS	13	9	11.31	4.11		Xp11.23	ubiquitin-activating enzyme E1 (A1S9T and BN75 temperature sensitivity complementing)	ubiquitin-activating enzyme E1 (A1S9T and BN75 temperature sensitivity complementing)
TETTRL	L11669_at	L11669	PASS	6	28.33	PASS	11	6	7.18	3.95		4p16.3	adducin 1 (alpha)	adducin 1 (alpha)
CSF3R	M59820_at	M59820	PASS	6	43.67	PASS	7	6	11.57	3.77		1p35-p34.3	colony stimulating factor 3 receptor (granulocyte)	colony stimulating factor 3 receptor (granulocyte)
IGF2	S73149_at	S73149	PASS	8	35.13	PASS	9	8	9.33	3.76			orf in intron 7 of insulin-like growth factor II gene	
18S3NAM	AFFX-HUM1	AFFX-HUM1	PASS	6	28.67	PASS	7	6	7.71	3.72				
18S3NA3	AFFX-HUM1	AFFX-HUM1	PASS	9	46.89	PASS	11	9	12.64	3.71				
PROTEIN_m	V01512_mal	V01512	PASS	9	51.44	PASS	13	9	13.92	3.69		14q24.3		v-fos FBJ murine osteosarcoma viral oncogene homolog
ETR101	M62831_at	M62831	PASS	9	105.67	PASS	13	9	28.69	3.68		19	immediate early protein	immediate early protein
DIA1	M28713_at	M28713	PASS	9	33.33	PASS	12	9	9.08	3.67		22q13.31-qter	cytochrome b5 reductase	diaphorase (NADH) (cytochrome b5 reductase)
MX1	M33882_at	M33882	PASS	7	34.71	PASS	9	7	9.56	3.63		21q22.3	myxovirus (influenza) resistance 1, homolog of murine (interferon-inducible protein p78)	myxovirus (influenza) resistance 1, homolog of murine (interferon-inducible protein p78)
SELPLG	U25956_at	U25956	PASS	9	75.89	PASS	13	9	21.08	3.60		12q24	selectin P ligand	selectin P ligand
LFP40	U72206_at	U72206	PASS	5	33.40	PASS	10	5	9.30	3.59		chr. 1	guanine nucleotide regulatory factor	guanine nucleotide regulatory factor
BB1	S82470_at	S82470	PASS	6	32.00	PASS	12	6	8.92	3.59				malignant cell expression-enhanced gene/humor progression-enhanced gene; This sequence comes from Fig. 4A
LYSPHADA	U56417_at	U56417	PASS	9	26.33	PASS	11	9	7.36	3.58			lysophosphatidic acid acyltransferase-alpha	LPAAT-4; 1-acyl-sn-glycerol-3-phosphate acyltransferase; similar to sequence within Class III MHC locus on chromosome 6 deposited in GenBank Accession Number U89336
HG4535-HT4	HG4535-HT4	HG4535-HT4	PASS	8	38.50	PASS	8	8	10.88	3.54				
ZYX	X95735_at	X95735	PASS	8	41.38	PASS	10	8	11.70	3.54		7q32	zyxin	zyxin
S71043_mal	S71043_mal	S71043	PASS	9	88.33	PASS	13	9	25.92	3.41			immunoglobulin A heavy chain allotype 2	This sequence comes from Fig. 3; IgA2 H chain
HD	L12392_at	L12392	PASS	9	22.33	PASS	9	9	6.56	3.41		4p16.3	huntingtin	huntingtin (Huntington disease)
ILK	U40282_at	U40282	PASS	9	29.22	PASS	12	9	8.58	3.40		11p15.5-p15.4	integrin-linked kinase	integrin-linked kinase
PKM2	X56494_at	X56494	PASS	8	63.50	PASS	13	8	18.77	3.38		15q22-qter	pyruvate kinase, muscle	pyruvate kinase, muscle
CD63_mal	X62654_mal	X62654	PASS	9	41.78	PASS	13	9	12.38	3.37		12q12-q13	CD63 antigen (melanoma 1 antigen)	CD63 antigen (melanoma 1 antigen)
SA	M60922_at	M60922	PASS	8	55.88	PASS	12	8	16.58	3.37		17q11-q12	flotillin 2	flotillin 2
X62083_s at	X62083_s at	X62083	PASS	9	70.89	PASS	13	9	21.15	3.35				

J03260_s_at	J03260_s_at	J03260	PASS	7	28.71	PASS	7	7	8.57	3.35	3.35	GNAZ	22q11.1-q11.2	guanine nucleotide binding protein (G protein), alpha z polypeptide	guanine nucleotide binding protein (G protein), alpha z polypeptide
CDC25	S78187_at	S78187	PASS	9	63.89	PASS	13	9	19.08	3.35	3.35	CDC25B	20p13	cell division cycle 25B	cell division cycle 25B
RELA	L19067_at	L19067	PASS	9	39.78	PASS	10	9	11.90	3.34	3.34			NF-kappa-B transcription factor subunit	putative
XQTP	D16469_at	D16469	PASS	9	31.67	PASS	11	9	9.55	3.32	3.32	ATP6S1	Xq28	ATPase, H+ transporting, lysosomal (vacuolar proton pump), subunit 1	ATPase, H+ transporting, lysosomal (vacuolar proton pump), subunit 1
RAGE_cds1	U89336_cds1	U89336	PASS	9	71.78	PASS	13	9	21.69	3.31	3.31	HBX2		homeobox PBX2 gene	intron-exon boundaries identified by a contig of ESTs with GenBank Accession Numbers W76064, R59617, W72507
K154_ADGT	D63876_at	D63876	PASS	9	33.89	PASS	12	9	10.25	3.31	3.31	KIAA0154			KIAA0154 gene product is related to mouse gamma adaptin.
PRSM1	U58048_at	U58048	PASS	8	18.63	PASS	9	8	5.67	3.29	3.29	PRSM1	16q24.3	protease, metallo, 1, 33kD	protease, metallo, 1, 33kD
ATP6C	M62762_at	M62762	PASS	9	69.67	PASS	13	9	21.23	3.28	3.28	ATP6C	16p13.3	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 16kD	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 16kD
NCF1	M55067_at	M55067	PASS	9	72.33	PASS	13	9	22.08	3.28	3.28	NCF1	7q11.23	neutrophil cytosolic factor 1	neutrophil cytosolic factor 1 (47kD, chronic granulomatous disease, autosomal 1)
K220	D86974_at	D86974	PASS	9	239.22	PASS	13	9	73.38	3.26	3.26	KIAA0220			
K109_CLASS	D63475_at	D63475	PASS	8	45.88	PASS	13	8	14.15	3.24	3.24	CLAPM1	3q28	clathrin-associated/assembly/adaptor protein, medium 1	clathrin-associated/assembly/adaptor protein, medium 1
TSC2	L48546_at	L48546	PASS	9	30.44	PASS	7	9	9.43	3.23	3.23	TSC2	16p13.3	tuberous sclerosis 2	tuberous sclerosis 2
EDR2	U89278_at	U89278	PASS	8	25.25	PASS	12	8	7.83	3.22	3.22	EDR2		early development regulator 2 (homolog of polyhomeotic 2)	early development regulator 2 (homolog of polyhomeotic 2)
M34996_s_at	M34996_s_at	M34996	PASS	9	80.56	PASS	13	9	25.08	3.21	3.21	PNUTL1	22q11.2	cell surface glycoprotein	cell surface glycoprotein
U59632_s_at	U59632_s_at	U59632	PASS	9	97.22	PASS	13	9	30.54	3.18	3.18	PNUTL1	22q11.2	peanut (Drosophila)-like 1	peanut (Drosophila)-like 1
UHX1	U44839_at	U44839	PASS	9	60.22	PASS	13	9	18.92	3.18	3.18	USP11	Xp21.2-p11.2	Ubiquitin carboxyl-terminal hydrolase, X-linked	ubiquitin specific protease 11
UKOD	X89267_at	X89267	PASS	5	47.60	PASS	8	5	15.25	3.12	3.12			uroporphyrinogen decarboxylase	
PLCB2	M95678_at	M95678	PASS	9	84.00	PASS	12	9	26.92	3.12	3.12	PLCB2	15q15	phospholipase C, beta 2	phospholipase C, beta 2
BST2	D28137_at	D28137	PASS	8	51.13	PASS	13	8	16.38	3.12	3.12	BST2	19p13.2	bone marrow stromal cell antigen 2	bone marrow stromal cell antigen 2
NFER2	S77763_at	S77763	PASS	9	32.33	PASS	11	9	10.36	3.12	3.12	nuclear factor erythroid 2 isoform f, transcription factor 1		nuclear factor erythroid 2 isoform f	basic leucine zipper protein; This sequence comes from Fig. 1; transcription factor 1NF-E2
EBVp	U19261_at	U19261	PASS	6	22.67	PASS	7	6	7.29	3.11	3.11			Epstein-Barr virus-induced protein	EBV induced protein
28SRNAM	AFFX-M278	AFFX-M278	PASS	5	91.00	PASS	7	5	29.29	3.11	3.11	GSTZ1	14q24.3	glutathione S-transferase Zeta 1	glutathione S-transferase Zeta 1
GSTZ1	U86529_at	U86529	PASS	9	25.56	PASS	11	9	8.27	3.09	3.09	GSTZ1	14q24.3	glutathione S-transferase Zeta 1	glutathione S-transferase Zeta 1
CD151	D29963_at	D29963	PASS	8	31.13	PASS	7	8	10.14	3.07	3.07	CD151	11p15.5	CD151 antigen	CD151 antigen
SAT_ma1	U40369_ma1	U40369	PASS	9	37.67	PASS	13	9	12.31	3.06	3.06	SAT	Xp22.1	spermidine/spermine N1-acetyltransferase	spermidine/spermine N1-acetyltransferase

CLU	M63379_at	M63379	PASS	9	222.78	PASS	13	9	72.85	3.06	3.06	CLU	8p21-p12	clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J)	clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J)
HMG1	D63874_at	D63874	PASS	9	83.22	PASS	13	9	27.31	3.05	3.05	HMG1	13q12	high-mobility group (nonhistone chromosomal) protein 1	high-mobility group (nonhistone chromosomal) protein 1
DEFA1	M26602_at	M26602	PASS	7	185.43	PASS	11	7	61.09	3.04	3.04	DEFA1	8p23.2-p23.1	defensin, alpha 1, myeloid-related sequence	defensin, alpha 1, myeloid-related sequence
FCGR1A	J04162_at	J04162	PASS	9	46.56	PASS	13	9	15.38	3.03	3.03	FCGR3A	1q23	Fe fragment of IgG, low affinity IIIa, receptor for (CD16)	Fe fragment of IgG, low affinity IIIa, receptor for (CD16)
M32304_s_a	M32304_s_at	M32304	PASS	8	26.75	PASS	13	8	8.85	3.02	3.02	TIMP2	17q25	tissue inhibitor of metalloproteinase 2	tissue inhibitor of metalloproteinase 2
LSP1	M33552_at	M33552	PASS	9	48.11	PASS	13	9	15.92	3.02	3.02	LSP1		lymphocyte-specific protein 1 (LSP1)	lymphocyte-specific protein 1 (LSP1)
U83239_s_at	U83239_s_at	U83239	PASS	6	34.33	PASS	11	6	11.36	3.02	3.02	GSTT1p28		CC chemokine STCP-1	CC chemokine STCP-1
GSTH	U90313_at	U90313	PASS	9	43.22	PASS	13	9	14.31	3.02	3.02	GSTT1p28		glutathione-S-transferase like	glutathione-S-transferase like
IGL1	U82275_at	U82275	PASS	8	27.88	PASS	12	8	9.25	3.01	3.01			immunoglobulin-like transcript 1	immunoglobulin-like transcript 1
NRGN_ma1	X99076_ma1	X99076	PASS	9	230.11	PASS	13	9	76.54	3.01	3.01	NRGN		neurogranin	neurogranin
UBA52	M26880_at	M26880	PASS	9	198.00	PASS	13	9	66.31	2.99	2.99	UBA52	19p13.1-p12	ubiquitin A-52 residue ribosomal protein fusion product 1	ubiquitin A-52 residue ribosomal protein fusion product 1
TMEM1	D26579_at	D26579	PASS	9	31.56	PASS	13	9	10.62	2.97	2.97	ADAM8	10q26.3	a disintegrin and metalloprotease domain 8	a disintegrin and metalloprotease domain 8
GPI	K03515_at	K03515	PASS	9	35.78	PASS	13	9	12.08	2.96	2.96	GPI	19q13.1	glucose phosphate isomerase	glucose phosphate isomerase
TYL	X99688_at	X99688	PASS	9	23.44	PASS	12	9	7.92	2.96	2.96	TYL		tyrosine-like	tyrosine-like
UBE1L	L13852_at	L13852	PASS	9	54.78	PASS	13	9	18.62	2.94	2.94	UBE1L	3p21	ubiquitin-activating enzyme E1, like	ubiquitin-activating enzyme E1, like
KRT1_ma1	M98776_ma1	M98776	PASS	7	19.29	PASS	9	7	6.56	2.94	2.94	KRT1		keratin 1	keratin 1
K45_YKL	D28476_at	D28476	PASS	9	27.44	PASS	12	9	9.33	2.94	2.94	TRIP12			thyroid hormone receptor interactor 12
HCF1	L20010_at	L20010	PASS	8	26.13	PASS	13	8	8.92	2.93	2.93	SLC9A1	1p36.1-p35	Na <sup>+</sup> /H <sup>+</sup> exchanger NHE-1 isoform	solute carrier family 9 (sodium/hydrogen exchanger), isoform 1 (antiporter, Na <sup>+</sup> /H <sup>+</sup> , amiloride sensitive)
SLC9A1	S68616_at	S68616	PASS	5	20.20	PASS	10	5	6.90	2.93	2.93	SLC9A1			small inducible cytokine A5 (RANTES)
SCYA5	M21121_at	M21121	PASS	9	156.78	PASS	13	9	53.69	2.92	2.92	SCYA5	17q11.2-q12	protein kinase, mitogen-activated, kinase 3 (MAP kinase 3)	protein kinase, mitogen-activated, kinase 3 (MAP kinase 3)
PRKMK3	D87116_at	D87116	PASS	9	32.89	PASS	11	9	11.27	2.92	2.92	PRKMK3	17q11.2	kinase kinase 3	kinase kinase 3
CCND3	M92287_at	M92287	PASS	9	68.33	PASS	13	9	23.62	2.89	2.89	CCND3	6p21	cyclin D3	cyclin D3
SMN1_ma2	U80017_ma2	U80017	PASS	8	18.38	PASS	11	8	6.36	2.89	2.89	btf2p44		basic transcription factor 2 p44	NAIP
PLCG2H	U45975_at	U45975	PASS	6	23.50	PASS	7	6	8.14	2.89	2.89			phosphatidylinositol (4,5)bisphosphate 5-phosphatase homolog	phosphatidylinositol (4,5)bisphosphate 5-phosphatase homolog
X74874_ma1	X74874_ma1	X74874	PASS	8	19.75	PASS	13	8	6.85	2.88	2.88			RNA polymerase II largest subunit	RNA polymerase II largest subunit
M36118_s_a	M36118_s_at	M36118	PASS	8	33.63	PASS	12	8	11.67	2.88	2.88	GZMB	14q11.2	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)

IMPDH1	J05272_at	J05272	PASS	9	31.44	PASS	13	9	10.92	2.88	2.88	IMPDH1	7q31.3-q32	IMP (inosine monophosphate) dehydrogenase 1
S40719_s at	S40719_s at	S40719	PASS	9	19.89	PASS	11	9	6.91	2.88	2.88	GFAP	17q21	glial fibrillary acidic protein
NAP1L4	U77456_at	U77456	PASS	6	29.50	PASS	12	6	10.25	2.88	2.88	ZNF162	11q13	nucleosome assembly protein 2
E_ZNF162	L49380_at	L49380	PASS	9	46.44	PASS	13	9	16.15	2.88	2.88	ZNF162	11q13	zinc finger protein 162
S100A12	D83657_at	D83657	PASS	9	65.44	PASS	13	9	22.77	2.87	2.87	CAAF1		calcium-binding protein in amniotic fluid 1
K56	D29954_at	D29954	PASS	8	18.88	PASS	7	8	6.57	2.87	2.87	KIAA0056		CHL1 protein
E_DDX11	U75968_at	U75968	PASS	9	20.56	PASS	12	9	7.17	2.87	2.87	CHL1		150 kDa oxygen-regulated protein ORP150
ORP150	U65785_at	U65785	PASS	9	33.67	PASS	12	9	11.75	2.87	2.87	ARF5	7q31.3	ADP-ribosylation factor 5
ARF5	M57567_at	M57567	PASS	8	46.00	PASS	13	8	16.15	2.85	2.85	PI6	6p25	protease inhibitor 6 (placental thrombin inhibitor)
S69272_s at	S69272_s at	S69272	PASS	9	24.67	PASS	13	9	8.69	2.84	2.84	MADD	11p11.21-p11.22	MAP-kinase activating death domain
AB002356_s	AB002356_s	AB002356	PASS	9	31.67	PASS	12	9	11.17	2.84	2.84	RGS2	1q31	regulator of G-protein signalling 2, 24kD
CSF1	HG1155-HT7	HG1155-H	PASS	8	27.63	PASS	9	8	9.78	2.83	2.83	UP	7	uridine phosphorylase
RGS2	L13391_at	L13391	PASS	9	60.33	PASS	13	9	21.38	2.82	2.82	KIAA0250		KIAA0250 gene product
UP	X90858_at	X90858	PASS	9	21.44	PASS	13	9	7.62	2.82	2.82	DF		D component of complement (adipsin)
K250	D87437_at	D87437	PASS	9	19.33	PASS	9	9	6.89	2.81	2.81	CDA	1p36.2-p35	cytidine deaminase
CNP_cds1	D13146_cds1	D13146	PASS	9	49.89	PASS	13	9	17.85	2.80	2.80	FAST		FAST kinase
CDA	L27943_at	L27943	PASS	6	32.33	PASS	10	6	11.60	2.79	2.79	CSK	15q23-q25	c-src tyrosine kinase
FAST	X86779_at	X86779	PASS	9	20.33	PASS	10	9	7.30	2.79	2.79	DF		D component of complement (adipsin)
X59932_s at	X59932_s at	X59932	PASS	9	62.44	PASS	13	9	22.46	2.78	2.78	CD33	19q13.3	CD33 antigen (gp67)
MAZ	M94046_at	M94046	PASS	9	29.67	PASS	13	9	10.69	2.77	2.77	ERF-2		ERF-2
DF	M84526_at	M84526	PASS	5	43.40	PASS	12	5	15.67	2.77	2.77	CLTA	12q23-q24	clathrin, light polypeptide (Lca)
PRKM3	D28915_at	D28915	PASS	7	16.00	PASS	10	7	5.80	2.76	2.76	MCL1	1q21	myeloid cell leukemia sequence 1 (BCL2-related)
CD33	M23197_at	M23197	PASS	8	21.00	PASS	13	8	7.62	2.76	2.76	calgizzarin		calgizzarin
D78577_s at	D78577_s at	D78577	PASS	9	85.67	PASS	13	9	31.08	2.76	2.76	TNFRSF1B	1p36.3-p36.2	tumor necrosis factor receptor 2 (75kD)
BRF2	X78992_at	X78992	PASS	8	64.88	PASS	13	8	23.54	2.76	2.76	NG10		guanine nucleotide binding protein 10
CLTA	M20471_at	M20471	PASS	9	73.36	PASS	13	9	26.69	2.76	2.76	POLR2E	19p13.3	polymrase (RNA) II (DNA directed) polypeptide E (25kD)
HG2868-HT1	HG2868-HT1	HG2868-H	PASS	7	18.57	PASS	12	7	6.75	2.75	2.75	KIAA0050		KIAA0050 gene product
MCL1	L08246_at	L08246	PASS	9	88.67	PASS	13	9	32.23	2.75	2.75	TGF-beta		transforming growth factor-beta
S100A11	D38583_at	D38583	PASS	9	81.00	PASS	13	9	29.54	2.74	2.74	BECN1		beclin 1 (coiled-coil, myosin-like BCL2-interacting protein)
TNFR2	M32315_at	M32315	PASS	9	67.44	PASS	13	9	24.62	2.74	2.74	AMPD2	1p13.3	adenosine monophosphate deaminase 2 (isoform L)
NG10	U31383_at	U31383	PASS	9	18.33	PASS	13	9	6.69	2.74	2.74			
D38251_s at	D38251_s at	D38251	PASS	8	30.75	PASS	13	8	11.23	2.74	2.74			
K50_K41	D30758_at	D30758	PASS	9	61.89	PASS	13	9	22.62	2.74	2.74			
M38449_s at	M38449_s at	M38449	PASS	6	33.50	PASS	8	6	12.25	2.73	2.73			
GT197	L38932_at	L38932	PASS	9	40.33	PASS	13	9	14.77	2.73	2.73			
AMPD2_cds	M91029_cds	M91029	PASS	9	30.33	PASS	13	9	11.15	2.72	2.72			

RABGGTA	Y08200_at	Y08200	PASS	9	23.56	PASS	12	9	8.67	2.72	2.72	RABGGTA	14q11.2	Rab geranylgeranyltransferase, alpha subunit	Rab geranylgeranyltransferase, alpha subunit
Y08682_mal	Y08682	Y08682	PASS	9	13.56	PASS	8	9	5.00	2.71	2.71	CPT1B		myosin, heavy polypeptide 9, non-muscle	myosin, heavy polypeptide 9, non-muscle
MYH9	M31013_at	M31013	PASS	9	149.78	PASS	13	9	55.38	2.70	2.70	MYH9	22q12.3-q13.1		
D00749_s at	D00749	D00749	PASS	9	69.89	PASS	13	9	25.85	2.70	2.70	MICB		CD7 antigen	MHC class I chain-related gene B; cDNA sequence deposited under GenBank Accession Number X91625
U65416_mal	U65416_mal	U65416	PASS	9	17.33	PASS	12	9	6.42	2.70	2.70			MHC class I molecule	
Z22951_mal	Z22951	Z22951	PASS	5	18.60	PASS	10	5	6.90	2.70	2.70	p65		p65 subunit of transcription factor NF-kappaB	
PRCC_mal	X99720_mal	X99720	PASS	7	22.43	PASS	9	7	8.33	2.69	2.69	TPRC			
HG2238-HT	HG2238-HT	HG2238-H	PASS	9	25.67	PASS	13	9	9.54	2.69	2.69	SLC2A3	12p13.3	soluble carrier family 2 (facilitated glucose transporter), member 3	
SLC2A3	M20681_at	M20681	PASS	9	26.00	PASS	12	9	9.67	2.69	2.69	FCGRT	19q13.3	Fc fragment of IgG, receptor, transporter, alpha	
FCGRT	U12255_at	U12255	PASS	9	78.56	PASS	13	9	29.23	2.69	2.69	LY6E	8q24.3	lymphocyte antigen 6 complex, locus E	
MAPT	HG2566-HT	HG2566-H	PASS	8	28.38	PASS	7	8	10.57	2.68	2.68	TNFRSF14	1p36.3-p36.2	tumor necrosis factor receptor superfamily, member 14; herpesvirus entry mediator	
EIFNGR2	U05875_at	U05875	PASS	8	34.88	PASS	8	8	13.00	2.68	2.68	YLF1	17q11.2	tetratricopeptide repeat domain 2	
TCF11	D43642_at	D43642	PASS	9	38.22	PASS	13	9	14.31	2.67	2.67	BTG2		protease inhibitor 1 (anti-elastase), alpha-1-antitrypsin	
U66711_mal	U66711_mal	U66711	PASS	8	48.75	PASS	12	8	18.25	2.67	2.67	BTG2		BTG2	rat PC3 and murine TIS21 genes homolog
HVEM	U70321_at	U70321	PASS	9	28.11	PASS	13	9	10.54	2.67	2.67	CSNK2A2	16p13.3-p13.2	casein kinase 2, alpha prime polypeptide	casein kinase 2, alpha prime polypeptide
TPR2	U46571_at	U46571	PASS	9	17.78	PASS	12	9	6.67	2.67	2.67	ARHG	11p15.5-p15.4	ras homolog gene family, member G (rho G)	ras homolog gene family, member G (rho G)
GARS	U09587_at	U09587	PASS	9	29.67	PASS	13	9	11.15	2.66	2.66	IRF3	19q13.3-q13.4	interferon regulatory factor 3	interferon regulatory factor 3
ARAF1	U01337_at	U01337	PASS	9	32.67	PASS	12	9	12.33	2.65	2.65	HEM1		HEM-1	
ISGF3G	M87503_at	M87503	PASS	8	52.50	PASS	13	8	19.85	2.65	2.65	NRAMP1	2q35	Nramp	natural resistance-associated macrophage protein 1 (might include Leishmaniasis)
PI	K01396_at	K01396	PASS	9	139.78	PASS	13	9	52.85	2.64	2.64	CLAPB1	17q11.2-q12	clathrin-associated/assembly/adaptor protein, large, beta 1	clathrin-associated/assembly/adaptor protein, large, beta 1
BTG2	U72649_at	U72649	PASS	9	40.33	PASS	12	9	15.25	2.64	2.64	KIAA0151		KIAA0151 gene product	KIAA0151 gene product
TXNRD1	U78678_at	U78678	PASS	8	20.25	PASS	9	8	7.67	2.64	2.64				
CSNK2A2	M55268_at	M55268	PASS	9	17.33	PASS	7	9	6.57	2.64	2.64				
ARHG	X61587_at	X61587	PASS	9	51.89	PASS	13	9	19.69	2.63	2.63				
IRF3	Z56281_at	Z56281	PASS	9	25.11	PASS	13	9	9.54	2.63	2.63				
HEM1	M58285_at	M58285	PASS	9	38.44	PASS	13	9	14.62	2.63	2.63				
NRAMP1	D50402_at	D50402	PASS	9	19.11	PASS	11	9	7.27	2.63	2.63				
CLAPB1	M34175_at	M34175	PASS	9	28.22	PASS	12	9	10.75	2.63	2.63				
ZFP77	HG4332-HT	HG4332-H	PASS	8	14.63	PASS	7	8	5.57	2.63	2.63				
K151_SPK1	D63485_at	D63485	PASS	9	18.89	PASS	10	9	7.20	2.62	2.62				

K226	D86979_at	D86979	PASS	9	20.56	PASS	13	9	7.85	2.62	2.62	KIAA0226			KIAA0226 gene product
BTN_mal	U97502_mal	U97502	PASS	6	16.50	PASS	13	6	6.31	2.62	2.62	BT3.3			butyrophilin
L32831_s_at	L32831_s_at	L32831	PASS	5	18.00	PASS	9	5	6.89	2.61	2.61				G protein-coupled receptor GPR3
FKBP4	M88279_at	M88279	PASS	9	23.11	PASS	13	9	8.85	2.61	2.61	FKBP4			FK506-binding protein 4 (59kD)
CTSD	M63138_at	M63138	PASS	9	82.89	PASS	12	9	31.75	2.61	2.61	CTSD			cathepsin D (lysosomal aspartyl protease)
HG2815-HT4	HG2815-HT4	HG2815-H	PASS	9	360.22	PASS	13	9	138.00	2.61	2.61				cathepsin D (lysosomal aspartyl protease)
L13939_s_at	L13939_s_at	L13939	PASS	8	24.88	PASS	13	8	9.54	2.61	2.61	ADTB1			adaplin, beta 1 (beta prime)
AOAH	M62840_at	M62840	PASS	8	27.50	PASS	9	8	10.56	2.61	2.61	AOAH			acyloxyacyl hydrolase (neutrophil)
TPR1	U46570_at	U46570	PASS	9	41.67	PASS	13	9	16.08	2.59	2.59	TTC1			tetratricopeptide repeat domain 1
TUBA1	X01703_at	X01703	PASS	9	37.67	PASS	13	9	14.54	2.59	2.59				alpha-tubulin
C5R1	M62505_at	M62505	PASS	8	25.00	PASS	12	8	9.67	2.59	2.59	C5R1			complement component 5 receptor 1 (C5a ligand)
U43185_s_at	U43185_s_at	U43185	PASS	9	27.56	PASS	12	9	10.67	2.58	2.58	STAT5A			signal transducer and activator of transcription 5A
AARS	D32050_at	D32050	PASS	8	19.38	PASS	12	8	7.50	2.58	2.58	AARS			alanyl-tRNA synthetase
SREBF1	U00968_at	U00968	PASS	6	24.67	PASS	7	6	9.57	2.58	2.58	SREBF1			sterol regulatory element binding transcription factor 1
GIP2	M13755_at	M13755	PASS	7	30.71	PASS	13	7	11.92	2.58	2.58	ISG15			interferon-stimulated protein, 15 kDa
BCAT2	U62739_at	U62739	PASS	9	18.78	PASS	10	9	7.30	2.57	2.57	BCAT2			branched chain aminotransferase 2, mitochondrial
DCTD	L39874_at	L39874	PASS	8	26.38	PASS	11	8	10.27	2.57	2.57	DCTD			dCMP deaminase
KL15_PPM1A	D13640_at	D13640	PASS	9	29.00	PASS	12	9	11.33	2.56	2.56	KIAA0015			KIAA0015 gene product
RTP	D87953_at	D87953	PASS	9	39.56	PASS	13	9	15.46	2.56	2.56	GC4			RTP
PXN	U14588_at	U14588	PASS	9	39.11	PASS	13	9	15.31	2.55	2.55	PXN			paxillin
KAP1_TIF1E	U95040_at	U95040	PASS	9	44.00	PASS	13	9	17.31	2.54	2.54	hKAP1/TIF1B			hKAP1/TIF1B
NRBTK	L20773_at	L20773	PASS	9	25.56	PASS	13	9	10.08	2.54	2.54				hyaluronoglucosaminidase 2
AJ000099_s	AJ000099_s	AJ000099	PASS	7	28.57	PASS	11	7	11.27	2.53	2.53	HYAL2			hyaluronoglucosaminidase 2
BZRP	L21954_at	L21954	PASS	9	127.89	PASS	13	9	50.46	2.53	2.53	BZRP			benzodiazepine receptor (peripheral)
HUK5	U67963_at	U67963	PASS	9	18.89	PASS	11	9	7.45	2.53	2.53	HUK5			lysophospholipase homolog
YF5	U84569_at	U84569	PASS	8	24.88	PASS	13	8	9.85	2.53	2.53	YF5			similar to A2 encoded by GenBank Accession Number U84570 and to sequence with GenBank Accession Number AC000020
STX5A	U26648_at	U26648	PASS	6	21.33	PASS	9	6	8.44	2.53	2.53	STX5A			synaptobrevin 5A
XG5784_s_at	XG5784_s_at	XG5784	PASS	8	21.88	PASS	12	8	8.67	2.52	2.52	CMAR			cell matrix adhesion regulator
SFCC13	L10910_at	L10910	PASS	9	16.11	PASS	13	9	6.38	2.52	2.52	CC1.3			splicing factor (CC1.3)
K79_CHIR7	D38555_at	D38555	PASS	9	21.33	PASS	10	9	8.50	2.51	2.51	KIAA0079			Sec24p, S. Cerevisiae, homolog of
E_A9A2BRB	U00952_at	U00952	PASS	5	17.80	PASS	10	5	7.10	2.51	2.51	NGK5			NGK5 protein
LAG2	M85276_at	M85276	PASS	9	138.22	PASS	13	9	55.15	2.51	2.51	PM1			pim-1 oncogene
M16750_s_at	M16750_s_at	M16750	PASS	9	34.89	PASS	13	9	13.92	2.51	2.51	PM1			pim-1 oncogene
K120_NP25	D21261_at	D21261	PASS	9	278.78	PASS	13	9	111.31	2.50	2.50	TAGLN2			transgelin 2
PRKACG	U42412_at	U42412	PASS	8	16.38	PASS	11	8	6.55	2.50	2.50	PRKAG1			protein kinase, AMP-activated, gamma 1 non-catalytic subunit

U41315_ma	U41315_ma	U41315	PASS	9	15.00	PASS	11	9	6.00	2.50	2.50	ZNF127-Xp	ZNF127-Xp	ring zinc-finger protein; escapes X chromosome inactivation
NFI16	HG3494-HT3	HG3494-H	PASS	9	80.56	PASS	13	9	32.23	2.50	2.50			
ANX11	L19605_at	L19605	PASS	9	97.56	PASS	13	9	39.08	2.50	2.50	ANX11	10q22-q23	annexin XI (56kD autoantigen)
K25	D14695_at	D14695	PASS	8	17.88	PASS	12	8	7.17	2.49	2.49	KIAA0025		KIAA0025 gene product
K144	DAG16	D63478	PASS	7	13.43	PASS	13	7	5.38	2.49	2.49	KIAA0144		KIAA0144 gene product
SI00A6	HG2788-HT2	HG2788-H	PASS	9	179.22	PASS	13	9	72.15	2.48	2.48			
PUTDNABP	U49278_at	U49278	PASS	8	27.63	PASS	13	8	11.15	2.48	2.48	UBE2V2		ubiquitin-conjugating enzyme E2 variant 2
HG3395-HT3	HG3395-HT3	HG3395-H	PASS	7	12.71	PASS	7	7	5.14	2.47	2.47			
BCL6	U00115_at	U00115	PASS	7	13.71	PASS	9	7	5.56	2.47	2.47	BCL6	3q27	B-cell CLL/lymphoma 6 (zinc finger protein 51)
SAFB	L43631_at	L43631	PASS	9	25.44	PASS	13	9	10.31	2.47	2.47	SAFB	19p13	scaffold attachment factor B
SRFGLYCP	Z50022_at	Z50022	PASS	8	32.00	PASS	13	8	13.00	2.46	2.46	C21ORF1	21q22.3	chromosome 21 open reading frame 1
MSN	M69066_at	M69066	PASS	9	178.78	PASS	13	9	72.85	2.45	2.45	MSN	Xq11.2-q12	moesin
PPP4C	X70218_at	X70218	PASS	7	27.43	PASS	11	7	11.18	2.45	2.45	PPP4C	16p12-16p11	protein phosphatase 4 (formerly X), catalytic subunit
EMP3	U52101_at	U52101	PASS	9	159.33	PASS	13	9	65.15	2.45	2.45	EMP3		epithelial membrane protein 3
TP11	HG2279-HT3	HG2279-H	PASS	9	73.33	PASS	13	9	30.00	2.44	2.44			
K121	D50911_at	D50911	PASS	9	16.44	PASS	11	9	6.73	2.44	2.44	KIAA0121		KIAA0121 gene product
M83652_s_a	M83652_s_a	M83652	PASS	9	46.56	PASS	13	9	19.08	2.44	2.44	PFC	Xp11.4	properdin P factor, complement
PLBK	U78095_at	U78095	PASS	5	26.40	PASS	11	5	10.82	2.44	2.44			member of the Kunitz family of protease inhibitors
FKBP1	M34539_at	M34539	PASS	9	42.78	PASS	13	9	17.54	2.44	2.44	FKBP1A	20p13	FK506-binding protein 1A (12kD)
SI00A4	M80563_at	M80563	PASS	9	213.22	PASS	13	9	87.62	2.43	2.43	SI00A4	1q12-q22	SI00 calcium-binding protein A4 (calcium protein, calvasculin, metastasin, murine placental homologue)
UQCRC1	L16842_at	L16842	PASS	9	24.11	PASS	12	9	9.92	2.43	2.43	UQCRC1	3p21	ubiquinol-cytochrome c reductase core protein 1
Y10807_s_a	Y10807_s_a	Y10807	PASS	7	35.14	PASS	13	7	14.46	2.43	2.43	HRMT1L2	19q13	HMT1 (hmRNP methyltransferase, S. cerevisiae)-like 2
SELP	M25322_at	M25322	PASS	9	15.00	PASS	11	9	6.18	2.43	2.43	SELP	1q22-q25	selectin P (granule membrane protein 140kD, antigen CD62)
PTGS1	M59979_at	M59979	PASS	8	15.25	PASS	7	8	6.29	2.43	2.43	PTGS1	9q32-q33.3	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)
PIL	U46751_at	U46751	PASS	9	98.78	PASS	13	9	40.77	2.42	2.42	P62		UBIQUITIN-BINDING PROTEIN P62, phosphotyrosine independent ligand for the Lck SH2 domain p62
ITPK1	U51336_at	U51336	PASS	9	49.00	PASS	13	9	20.23	2.42	2.42			inositol 1,3,4-trisphosphate 5/6-kinase
KNS2	L04733_at	L04733	PASS	7	17.29	PASS	7	7	7.14	2.42	2.42			kinesin light chain
M23323_s_a	M23323_s_a	M23323	PASS	9	45.78	PASS	13	9	18.92	2.42	2.42	CD3E	11q23	CD3E antigen, epsilon polypeptide (TfT3 complex)
X76223_s_a	X76223_s_a	X76223	PASS	7	36.86	PASS	12	7	15.25	2.42	2.42	MAL	2cen-q13	mal, T-cell differentiation protein

OS9	U41635_at	U41635	PASS	9	58.56	PASS	13	9	24.23	2.42	2.42			OS-9 precursor	ubiquitously expressed in human tissues and amplified in sarcomas
RPS6KA2	L07597_at	L07597	PASS	9	28.78	PASS	12	9	11.92	2.41	2.41	3	RPS6KA1	ribosomal protein S6 kinase, 90kD, polypeptide 1	ribosomal protein S6 kinase, 90kD, polypeptide 1
IFNG	L07633_at	L07633	PASS	9	84.33	PASS	13	9	34.92	2.41	2.41	14q11.2	PSME1	interferon-gamma	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)
FRAPL	L37033_at	L37033	PASS	8	29.38	PASS	11	8	12.18	2.41	2.41		FKBP38	FK-506 binding protein	
CES1	L07765_at	L07765	PASS	7	15.43	PASS	10	7	6.40	2.41	2.41	16q13-q22.1	CES1	carboxylesterase 1 (monocyte/macrophage serine esterase 1)	carboxylesterase 1 (monocyte/macrophage serine esterase 1)
X56681 s at	X56681 s at	X56681	PASS	9	114.44	PASS	13	9	47.54	2.41	2.41	19p13.2	JUND	jun D protein	jun D proto-oncogene
HDLBP	M64098_at	M64098	PASS	8	20.00	PASS	13	8	8.31	2.41	2.41		HBP	high density lipoprotein binding protein	
ECGF1_ma3	U62317_ma3	U62317	PASS	9	66.22	PASS	13	9	27.54	2.40	2.40			arylsulfatase A	hypothetical protein 384D8_2
K140	D50930_at	D50930	PASS	8	18.13	PASS	11	8	7.55	2.40	2.40		KIAA0140		KIAA0140 gene product
HG4541-HT4	HG4541-HT4	HG4541-HT4	PASS	9	41.56	PASS	13	9	17.31	2.40	2.40				
ARP	M83751_at	M83751	PASS	9	21.22	PASS	13	9	8.85	2.40	2.40		ARP	arginine-rich protein	putative
HG417-HT4	HG417-HT4	HG417-HT4	PASS	9	71.33	PASS	13	9	29.77	2.40	2.40				
STM	U20499_at	U20499	PASS	9	20.33	PASS	12	9	8.50	2.39	2.39	16p11.2	SULT1A3	thermolabile phenol sulfotransferase	sulfotransferase family 1A, phenol-preferring, member 3
NP	K02574_at	K02574	PASS	8	32.88	PASS	13	8	13.77	2.39	2.39	14q11.2	NP	nucleoside phosphorylase	nucleoside phosphorylase
GLA	X14448_at	X14448	PASS	9	20.56	PASS	13	9	8.62	2.39	2.39			alpha-D-galactosidase A	
ARNP	M74002_at	M74002	PASS	9	20.00	PASS	13	9	8.38	2.39	2.39	1p21-p34	SFRS11	splicing factor, arginine/serine-rich 11	splicing factor, arginine/serine-rich 11
K168	D79990_at	D79990	PASS	9	29.33	PASS	13	9	12.31	2.38	2.38		KIAA0168	suppressor of Ty (S.cerevisiae) 4 homolog 1	KIAA0168 gene product
SUPT4H1	D43923_at	D43923	PASS	8	21.63	PASS	12	8	9.08	2.38	2.38	17q21-q23	SUPT4H1	suppressor of Ty (S.cerevisiae) 4 homolog 1	suppressor of Ty (S.cerevisiae) 4 homolog 1
K174	D79996_at	D79996	PASS	9	28.56	PASS	13	9	12.00	2.38	2.38		KIAA0174	D-dopachrome tautomerase	KIAA0174 gene product
DC1	U49785_at	U49785	PASS	9	24.89	PASS	13	9	10.46	2.38	2.38	22q11.2	DDT	D-dopachrome tautomerase	D-dopachrome tautomerase
CLP36	U90878_at	U90878	PASS	9	26.56	PASS	12	9	11.17	2.38	2.38	10q22-q27	CLIM1	carboxyl terminal LIM domain protein	carboxy terminal LIM domain protein 1
LAMP5	U51240_at	U51240	PASS	9	146.89	PASS	13	9	61.77	2.38	2.38		LAPTM5	lysosomal-associated multitransmembrane protein	
NK4	M59807_at	M59807	PASS	9	116.67	PASS	13	9	49.15	2.37	2.37	16p13.3	NK4	natural killer cell transcript 4	natural killer cell transcript 4
K223_COSZ	D86976_at	D86976	PASS	9	103.11	PASS	13	9	43.46	2.37	2.37		KIAA0223		similar to C.elegans protein (Z37093)
B94	M92357_at	M92357	PASS	9	27.00	PASS	13	9	11.38	2.37	2.37			B94 protein	secreted protein, acidic, cysteine-rich (osteonecin)
SPARC	J03040_at	J03040	PASS	9	57.78	PASS	13	9	24.38	2.37	2.37	5q31-q33	SPARC	secreted protein, acidic, cysteine-rich (osteonecin)	secreted protein, acidic, cysteine-rich (osteonecin)
PPGB	M22960_at	M22960	PASS	9	83.44	PASS	13	9	35.23	2.37	2.37	20q13.1	PPGB	protective protein for beta-galactosidase	protective protein for beta-galactosidase (galactosialidosis)
MX2	M30818_at	M30818	PASS	9	20.56	PASS	13	9	8.69	2.36	2.36	21q22.3	MX2	interferon-induced Mx protein	myxovirus (influenza) resistance 2, homolog of murine
SMRT	U37146_at	U37146	PASS	9	26.56	PASS	13	9	11.23	2.36	2.36		SMRT	silencing mediator of retinoid and thyroid hormone action	transcriptional co-repressor
DGK5Z	U51477_at	U51477	PASS	9	32.56	PASS	13	9	13.77	2.36	2.36		DGKZ	diacylglycerol kinase, zeta (104kD)	diacylglycerol kinase, zeta (104kD)
LAMP1	J04182_at	J04182	PASS	9	47.78	PASS	13	9	20.23	2.36	2.36		LAMP1	lysosomal membrane glycoprotein-1	precursor
YWHAE	U54778_at	U54778	PASS	8	14.50	PASS	13	8	6.15	2.36	2.36			14-3-3 epsilon	
U51333 s at	U51333 s at	U51333	PASS	9	47.11	PASS	13	9	20.00	2.36	2.36	5q35.2	HK3	hexokinase 3 (white cell)	hexokinase 3 (white cell)



CRFB4 PIM2	Z17227_at U77735_at	Z17227 U77735	PASS PASS	9 6	15.78 24.33	PASS PASS	10 12	9 6	6.70 10.33	2.35 2.35	IL10RB	21q22.1-q22.2	interleukin 10 receptor, beta pim-2 protooncogene homolog pim-2h	interleukin 10 receptor, beta similar to murine pim-2 product encoded by GenBank Accession Number L41495; serine/threonine protein kinase
AAMP	M95627_at	M95627	PASS	9	22.11	PASS	12	9	9.42	2.35	AAMP		angio-associated, migratory cell protein	
K67_TOIP2 NKG2D	D31891_at X54870_at	D31891 X54870	PASS PASS	9 9	18.56 31.33	PASS PASS	11 13	9 9	7.91 13.38	2.35 2.34	KIAA0067 NKG2-D gene		KIAA0067 gene product Type II integral membrane protein	
M81695_s_a	M81695_s_a	M81695	PASS	9	32.22	PASS	13	9	13.77	2.34	ITGAX	16p13.1-p11	integrin, alpha X (antigen CD11C (p150), alpha polypeptide)	
KRT12	U77643_at	U77643	PASS	8	28.25	PASS	13	8	12.08	2.34	SECTM1	17q25	secreted and transmembrane 1 lectin, galactoside-binding, soluble, 9 (galectin 9)	
LGALS9	AB006782_a	AB006782	PASS	9	78.89	PASS	13	9	33.77	2.34	LGALS9		lectin, galactoside-binding, soluble, 9 (galectin 9)	
ARF3	M74491_at	M74491	PASS	9	54.11	PASS	13	9	23.23	2.33	ARF3	12q13	ADP-ribosylation factor 3	
ALDH7	U10868_at	U10868	PASS	8	16.88	PASS	12	8	7.25	2.33	ALDH7	11q13	aldehyde dehydrogenase 7	
M54915_s_a	M54915_s_a	M54915	PASS	9	54.67	PASS	13	9	23.54	2.32			pim-1 protein	
FAH	M55150_at	M55150	PASS	6	18.50	PASS	8	6	8.00	2.31	FAH	15q23-q25	fumarylacetoacetate	
TPM3	HG3514-HTT	HG3514-H	PASS	9	149.22	PASS	13	9	64.54	2.31			protein tyrosine kinase 2 beta	
CAKB	U43522_at	U43522	PASS	8	14.13	PASS	9	8	6.11	2.31	PTK2B	8p21.1	intercellular adhesion molecule 3	
ICAM3	X69819_at	X69819	PASS	9	52.22	PASS	13	9	22.62	2.31	ICAM3	19p13.3-p13.2	interferon regulatory factor 5 adenylyl cyclase-associated protein	
IRF5	U51127_at	U51127	PASS	9	29.00	PASS	7	9	12.57	2.31	IRF5	7q32	TATA box binding protein (TBP)- associated factor, RNA polymerase II, N, 68kD (RNA-binding protein 56)	
CAP	L12168_at	L12168	PASS	9	134.67	PASS	13	9	58.38	2.31	CAP		70 kDa	
RBP56	U51334_at	U51334	PASS	8	25.50	PASS	13	8	11.08	2.30	TAF2N	17q11.1-q11.2	Protein sequence is in conflict with the conceptual translation.	
HSPA1L_ma	M11717_ma	M11717	PASS	9	53.11	PASS	13	9	23.08	2.30	HSPA1L		no similarities to reported gene products	
RGL2	U68142_at	U68142	PASS	9	15.67	PASS	11	9	6.82	2.30	RGL2		capping protein (actin filament), gelsolin-like	
PM5	X57398_at	X57398	PASS	9	27.33	PASS	12	9	11.92	2.29	PM5		NIMA-interacting protein 1, essential mitotic regulator, essential peptidyl-prolyl isomerase	
K217	D86971_at	D86971	PASS	5	17.20	PASS	10	5	7.50	2.29	KIAA0217		zipper protein	
CAPG	M94345_at	M94345	PASS	9	49.33	PASS	13	9	21.54	2.29	CAPG	2cen-q24	integrin, alpha M (complement component receptor 3, alpha; also known as CD11b (p170), macrophage antigen alpha polypeptide)	
PIN1	U49070_at	U49070	PASS	6	14.50	PASS	12	6	6.33	2.29	PIN1		RasGAP-related protein	
U72882_s_at	U72882_s_at	U72882	PASS	6	15.50	PASS	9	6	6.78	2.29	IFP35		IQGAP2; Cdc42-, Rac1-, and calmodulin-binding protein	
ITGAM	J03925_at	J03925	PASS	9	23.56	PASS	13	9	10.31	2.29	ITGAM	16p11.2		
IQGAP2	U51903_at	U51903	PASS	8	17.38	PASS	13	8	7.62	2.28	IQGAP2			

MLN62	X80200_at	X80200	PASS	9	15.11	PASS	8	9	6.63	2.28	2.28	17q11-q12	TNF receptor-associated factor 4	TNF receptor-associated factor 4
INPP5D	U57650_at	U57650	PASS	9	42.78	PASS	13	9	18.77	2.28	2.28	2q36-q37	inositol polyphosphate-5-phosphatase, 145kD	inositol polyphosphate-5-phosphatase, 145kD
M13829_s_at	M13829_s_at	M13829	PASS	8	15.25	PASS	13	8	6.69	2.28	2.28	Xp11.4-p11.2	v-raf murine sarcoma 3611 viral oncogene homolog 1	v-raf murine sarcoma 3611 viral oncogene homolog 1
ITGB2	M15395_at	M15395	PASS	9	86.11	PASS	13	9	37.85	2.28	2.28	21q22.3	integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit)	integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit)
D43682_s_at	D43682_s_at	D43682	PASS	9	41.44	PASS	13	9	18.23	2.27	2.27	17p13-p11	acyl-Coenzyme A dehydrogenase, very long chain	acyl-Coenzyme A dehydrogenase, very long chain
FTH1	L20941_at	L20941	PASS	9	279.00	PASS	13	9	122.77	2.27	2.27	11q13	ferritin, heavy polypeptide 1	ferritin, heavy polypeptide 1
PSMHC9	D00763_at	D00763	PASS	9	42.78	PASS	12	9	18.83	2.27	2.27	PSMA4	proteasome (prosome, macropain) subunit, alpha type, 4	proteasome (prosome, macropain) subunit, alpha type, 4
AKT1	M63167_at	M63167	PASS	8	23.13	PASS	11	8	10.18	2.27	2.27	14q32.3	rac protein kinase-alpha	rac protein kinase-alpha
POGA	L24783_at	L24783	PASS	7	14.29	PASS	10	7	6.30	2.27	2.27		anti-oxidant protein 2 (non-selenium glutathione peroxidase, acidic calcium-independent phospholipase A2)	anti-oxidant protein 2 (non-selenium glutathione peroxidase, acidic calcium-independent phospholipase A2)
K106_B15C	D14662_at	D14662	PASS	9	36.44	PASS	13	9	16.08	2.27	2.27	1	guanine nucleotide exchange factor; 115-kD, mouse Lsc homolog	guanine nucleotide exchange factor; 115-kD, mouse Lsc homolog
CYP2A6_f	X13930_f	X13930	PASS	5	13.60	PASS	9	5	6.00	2.27	2.27		P-450 IIA4 protein (AA 1-494)	P-450 IIA4 protein (AA 1-494)
K113	D30755_at	D30755	PASS	9	29.11	PASS	13	9	12.85	2.27	2.27	KIAA0113	transaldolase	transaldolase
P115RHOG	U64105_at	U64105	PASS	9	43.56	PASS	13	9	19.23	2.26	2.26	SUB1.5	proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	proteasome (prosome, macropain) 26S subunit, non-ATPase, 2
TALDO1	L19437_at	L19437	PASS	9	85.33	PASS	13	9	37.69	2.26	2.26		lectin, galactoside-binding, soluble, 1 (galactin 1)	lectin, galactoside-binding, soluble, 1 (galactin 1)
PSMD2	D78151_at	D78151	PASS	9	36.22	PASS	13	9	16.00	2.26	2.26	PSMD2	ubiquitin fusion-degradation 1 like protein	ubiquitin fusion-degradation 1 like protein
LGALS1	J04456_at	J04456	PASS	9	102.89	PASS	13	9	45.46	2.26	2.26	22q12-q13	pre-B-cell leukemia transcription factor 1	pre-B-cell leukemia transcription factor 1
UFD1L	U64444_at	U64444	PASS	9	22.78	PASS	13	9	10.08	2.26	2.26		hal1025 is new	hal1025 is new
K68	D38549_at	D38549	PASS	8	19.63	PASS	10	8	8.70	2.26	2.26	KIAA0068	pre-B-cell leukemia transcription factor 1	pre-B-cell leukemia transcription factor 1
PBX1	M86546_at	M86546	PASS	6	12.50	PASS	11	6	5.55	2.25	2.25	PBX1	protein kinase, mitogen-activated, kinase 2, p45 (MAP kinase kinase 2)	protein kinase, mitogen-activated, kinase 2, p45 (MAP kinase kinase 2)
RAC2	HG1102-HT	HG1102-HT	PASS	9	20.11	PASS	13	9	8.92	2.25	2.25		This gene is novel	This gene is novel
PRKMK2	L11285_at	L11285	PASS	9	29.11	PASS	13	9	12.92	2.25	2.25		paired basic amino acid cleaving system 4	paired basic amino acid cleaving system 4
K82_ACPN	D43949_at	D43949	PASS	8	16.75	PASS	11	8	7.45	2.25	2.25	KIAA0082	This sequence comes from Fig. 3.	This sequence comes from Fig. 3.
PACE4	M80482_at	M80482	PASS	7	11.71	PASS	9	7	5.22	2.24	2.24	PACE4		
GMCSFIND	S69115_at	S69115	PASS	8	80.38	PASS	13	8	35.85	2.24	2.24	granulocyte colony-stimulating factor induced gene		

ZAP70	L05148_at	L05148	PASS	9	36.56	PASS	13	9	16.31	2.24	2.24	NC2			alpha subunit; forms heterodimer with NC2 alpha/Dr1
X96506_s_at	X96506_s_at	X96506	PASS	5	22.40	PASS	10	5	10.00	2.24	2.24				
BRCA2	U05035_at	U05035	PASS	9	15.67	PASS	12	9	7.00	2.24	2.24				
PPP2R1A	J02902_at	J02902	PASS	8	33.38	PASS	12	8	14.92	2.24	2.24				phosphatase 2A regulatory subunit
IL2RB	M26062_at	M26062	PASS	8	35.25	PASS	13	8	15.77	2.24	2.24	IL2RB	22q13		interleukin 2 receptor, beta
DJ1	D61380_at	D61380	PASS	9	58.44	PASS	13	9	26.15	2.23	2.23				DJ-1 protein
UBL1	D23662_at	D23662	PASS	9	53.11	PASS	13	9	23.77	2.23	2.23				ubiquitin-like protein
ZNF173	U09825_at	U09825	PASS	9	21.44	PASS	13	9	9.62	2.23	2.23	ZNF173	6p21.3		zinc finger protein 173
UCP2	U94592_at	U94592	PASS	9	50.22	PASS	13	9	22.54	2.23	2.23	UCPH			uncoupling protein homolog
L35249_s_at	L35249_s_at	L35249	PASS	9	33.89	PASS	13	9	15.23	2.23	2.23	ATP6B2			ATPase, H+ transporting, lysosomal (vacuolar proton pump), beta polypeptide, 56/58kD, isoform 2
SLA	D89077_at	D89077	PASS	9	31.89	PASS	12	9	14.33	2.22	2.22				Src-like adapter protein
TUBB2	HG1980-HT7	HG1980-HT7	PASS	9	53.22	PASS	13	9	23.92	2.22	2.22				
K88	D42041_at	D42041	PASS	9	21.56	PASS	13	9	9.69	2.22	2.22	KIAA0088			The ha1225 gene product is related to human alpha-glucosidase.
GUSB	M15182_at	M15182	PASS	9	18.89	PASS	12	9	8.50	2.22	2.22	GUSB	7q22		glucuronidase, beta
RAD23A	D21235_at	D21235	PASS	9	15.56	PASS	10	9	7.00	2.22	2.22	RAD23A	19p13.2		RAD23 (S cerevisiae) homolog A
TRAIL	U37518_at	U37518	PASS	9	34.44	PASS	13	9	15.54	2.22	2.22	TNFSF10	3q26		tumor necrosis factor (ligand) superfamily, member 10
UNP	U20657_at	U20657	PASS	9	14.78	PASS	12	9	6.67	2.22	2.22	USP4	3p21.3		ubiquitin specific protease, proto-oncogene
PDIP5	D49489_at	D49489	PASS	9	19.22	PASS	13	9	8.69	2.21	2.21				The transcript is amplified in hydroxyurea-resistant cells; an endoplasmic reticulum-retention signal (ER-retention signal) at 1403-1414; two thioredoxin-like sequences (Trx-like motifs) at 254-271, 659-676
OGDH	D10523_at	D10523	PASS	7	13.57	PASS	7	7	6.14	2.21	2.21	OGDH	7p13-p11.2		oxoglutarate dehydrogenase (lipoamide)
PALMPH	U44772_at	U44772	PASS	9	26.00	PASS	13	9	11.77	2.21	2.21	PPT	1p32		palmitoyl-protein thioesterase (ceroid-lipofuscinosis, neuronal 1, infantile; Hattia-Santavuori disease)
ATPLP	D89052_at	D89052	PASS	9	53.11	PASS	13	9	24.08	2.21	2.21	ATP6F	1p32.3		ATPase, H+ transporting, lysosomal (vacuolar proton pump) 21kD
FGR	M19722_at	M19722	PASS	9	94.78	PASS	13	9	43.00	2.20	2.20	FGR	1p36.2-p36.1		Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog
PCMT1	D25547_at	D25547	PASS	9	13.22	PASS	9	9	6.00	2.20	2.20				PCMT isozyme 1
NCF2	M32011_at	M32011	PASS	9	53.22	PASS	13	9	24.23	2.20	2.20	NCF2	1cen-q32		neutrophil cytosolic factor 2 (65kD, chronic granulomatous disease, autosomal 2)
HG998-HT99	HG998-HT99	HG998-HT99	PASS	9	21.00	PASS	12	9	9.58	2.19	2.19				
K218_HYP2	D86972_at	D86972	PASS	9	13.78	PASS	10	9	6.30	2.19	2.19	KIAA0218			KIAA0218 gene product
H2A2	L19779_at	L19779	PASS	9	71.89	PASS	13	9	32.92	2.18	2.18	H2AFO			H2A histone family, member O

Z47038_s at Z47038_s at	Z47038_s at	Z47038_s at	8	12.88	PASS	11	8	5.91	2.18	2.18	putative microtubule associated protein 1A			open reading frame; N-terminal region
K224 DDX	D86977 at	D86977	8	15.25	PASS	13	8	7.00	2.18	2.18	KIAA0224			KIAA0224 gene product
K160	D63881 at	D63881	9	14.56	PASS	13	9	6.69	2.17	2.17	KIAA0160			KIAA0160 gene product is novel.
D83260_s at	D83260_s at	D83260	9	16.56	PASS	13	9	7.62	2.17	2.17	DXS9928E	Xq28		putative candidate disease gene
EIF3	U78525 at	U78525	9	19.56	PASS	13	9	9.00	2.17	2.17	EIF3S9			XAP5
K169	D79991 at	D79991	9	13.67	PASS	10	9	6.30	2.17	2.17	KIAA0169			eukaryotic translation initiation factor 3, subunit 9 (eta, 116kD)
GZMA_ma1	M18737_ma	M18737	9	75.22	PASS	13	9	34.69	2.17	2.17	GZMA	5q11-q12		putative hydrophobic domain in amino acid positions 373-390.
PP1	U14603 at	U14603	9	76.56	PASS	13	9	35.31	2.17	2.17	P1P4A2	1p35		granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3)
MLF2	U57342 at	U57342	9	26.00	PASS	13	9	12.00	2.17	2.17	MLF2			protein tyrosine phosphatase type IVA, member 2
M84371_ma	M84371_ma	M84371	8	14.38	PASS	11	8	6.64	2.17	2.17	CD19			myelodysplasia/myeloid leukemia factor 2
H1X	D64142 at	D64142	9	54.89	PASS	13	9	25.38	2.16	2.16	H1FX			histone H1x
CMKBR2_m	U95626_ma	U95626	8	36.75	PASS	13	8	17.00	2.16	2.16	ccr2			confirmed by similarity to Human monocyte chemoattractant protein 1 receptor (ccr2) alternatively spliced A-form, Encoded by GenBank Accession Number U80924, gi 1168965
U32986_s at	U32986_s at	U32986	9	24.67	PASS	12	9	11.42	2.16	2.16	DDB1	11q12-q13		damage-specific DNA binding protein 1 (127kD)
MPP1	M64925 at	M64925	9	34.89	PASS	12	9	16.17	2.16	2.16	MPP1	Xq28		membrane protein, palmitoylated 1 (55kD)
BCL2	M14745 at	M14745	9	16.22	PASS	13	9	7.54	2.15	2.15				bel-2 protein
DAGK1	X62535 at	X62535	9	38.56	PASS	13	9	17.92	2.15	2.15	DGKA	12		diacylglycerol kinase, alpha (80kD)
M63438_s at	M63438_s at	M63438	9	167.11	PASS	13	9	77.77	2.15	2.15				
TRADD	L41690 at	L41690	9	18.00	PASS	13	9	8.38	2.15	2.15	TRADD			TNFRSF1A-associated via death domain
PGM1	M83088 at	M83088	9	16.67	PASS	13	9	7.77	2.15	2.15	PGM1	1p22.1		phosphoglucomutase 1
CRIP1	U09770 at	U09770	9	35.33	PASS	12	9	16.50	2.14	2.14	ICRHP			cysteine-rich heart protein
K43_HOM	D26362 at	D26362	8	17.13	PASS	9	8	8.00	2.14	2.14	KIAA0043			KIAA0043 gene product
MYD88	U70451 at	U70451	8	38.13	PASS	13	8	17.85	2.14	2.14	MYD88	3p22		myeloid differentiation primary response gene (88)
HNRPH1	L22009 at	L22009	9	74.00	PASS	13	9	34.69	2.13	2.13				49 kDa protein; heterogeneous nuclear ribonucleoprotein H
MXI1	L07648 at	L07648	9	17.56	PASS	13	9	8.23	2.13	2.13	MXI1			
GUKE1	L76200 at	L76200	8	56.25	PASS	13	8	26.38	2.13	2.13	GUKE1	1q32-q42		guanylate kinase 1
CSFWPH	AJ00480 at	AJ00480	5	11.60	PASS	9	5	5.44	2.13	2.13	CSFW			phosphoprotein
GNG11	U31384 at	U31384	9	38.78	PASS	13	9	18.23	2.13	2.13	GNG11			guanine nucleotide binding protein 11
HG3076-HT3	HG3076-HT3	HG3076-HT3	9	52.33	PASS	13	9	24.62	2.13	2.13				
UGT2B4	U03105 at	U03105	7	19.86	PASS	11	7	9.36	2.12	2.12				IB4-2 protein





ETR3	U69546_at	U69546	PASS	7	22.71	PASS	13	7	11.15	2.04	2.04	Etr-3	protein contains 3 RRM motifs that may bind RNA; putative RNA binding protein; Elav-type ribonucleoprotein; complete sequence of human EST, GenBank Accession Number R57293
GSK3A	L40027_at	L40027	PASS	9	19.89	PASS	13	9	9.77	2.04	2.04	glycogen synthase kinase 3	exon 1 part (leader region) bp6-77; exon 2 part (alpha-1 domain): bp78-347; exon 3 part (alpha-2 domain): bp348-623; exon 4 part (alpha-3 domain): bp624-899; exon 5 part (transmembrane region): bp900-1016; exon 6 part (cytoplasmic region): bp1017-1049; exon 7 part (cytoplasmic region): bp1050-1097; exon 8 part (cytoplasmic region): bp1098-1103
HLA-A_f	D32129_f_at	D32129	PASS	9	342.11	PASS	13	9	168.23	2.03	2.03	HLA-A26	
RB1	L22343_at	L22343	PASS	7	12.86	PASS	9	7	6.33	2.03	2.03	nuclear phosphoprotein	IFN-induced phosphatidylinositol 4-kinase, catalytic, alpha polypeptide
PIK4	L36151_at	L36151	PASS	9	39.89	PASS	13	9	19.69	2.03	2.03	PIK4CA	phosphatidylinositol 4-kinase, catalytic, alpha polypeptide
SPS2	U43286_at	U43286	PASS	9	13.67	PASS	12	9	6.75	2.02	2.02	SPS2	is a selenocysteine encoded by the TGA (UGA) codon: We designated this enzyme selenophosphate synthetase 2 to distinguish it from the human homolog described by Low, S.C., Harney, J.W. and Berry, M.J. J. Biol. Chem. 270, 21659-21664 (1995) (GenBank Accession Number U34044)
HYPA	U81556_at	U81556	PASS	9	40.44	PASS	13	9	20.00	2.02	2.02	hypothetical protein A4	mitogen-activated protein kinase-activated protein kinase 3
3PK	U09578_at	U09578	PASS	8	17.25	PASS	13	8	8.54	2.02	2.02	MAPKAPK3	mitogen-activated protein kinase-activated protein kinase 3
K23_CAN	D14689_at	D14689	PASS	9	32.11	PASS	12	9	15.92	2.02	2.02	KIAA0023	KIAA0023 gene product
RNA_OSTB	AB000115_a	AB000115	PASS	7	12.86	PASS	8	7	6.38	2.02	2.02		The submitters designated this product as G53686
IL2RG	D11086_at	D11086	PASS	9	42.00	PASS	13	9	20.85	2.01	2.01	IL2RG	interleukin 2 receptor, gamma (severe combined immunodeficiency)
SEC14L	D67029_at	D67029	PASS	5	15.60	PASS	12	5	7.75	2.01	2.01	SEC14L	SEC14 (S. cerevisiae)-like
POLG	U60325_at	U60325	PASS	6	13.33	PASS	8	6	6.63	2.01	2.01	POLG	polymerase (DNA directed), gamma
K142_K6	D63476_at	D63476	PASS	9	14.22	PASS	13	9	7.08	2.01	2.01	P85SPR	PAK-interacting exchange factor beta
FCGR1A	M63835_at	M63835	PASS	7	12.29	PASS	8	7	6.13	2.01	2.01	FCGR1A	Fe fragment of IgG, high affinity Ia, receptor for (CD64)
MLK3	L32976_at	L32976	PASS	7	12.29	PASS	7	7	6.14	2.00	2.00	MLK3	mixed lineage kinase 3
E_CCA12	U06681_at	U06681	PASS	5	12.40	PASS	10	5	6.20	2.00	2.00		

FACLI	D10040_at	D10040	PASS	5	12.00	PASS	9	5	6.00	2.00	2.00	FACLI	3q13	fatty-acid-Coenzyme A ligase, long-chain 1	fatty-acid-Coenzyme A ligase, chain 1
MCM6	D84557_at	D84557	PASS	9	13.44	PASS	11	9	6.73	2.00	2.00			HsMcm6	
PASCA2	U50523_at	U50523	PASS	9	84.89	PASS	13	9	42.54	2.00	2.00				
BIOC3	AFFX-BIOC-AFFX-BIOC	fail	fail	4		PASS	13	4	14.46	Normal	Normal				
L15189_s_at	L15189_s_at	L15189	fail	4		PASS	13	4	6.77	Normal	Normal	HSPA9B	5q31.1	heat shock 70kD protein 9B (mortalin-2)	heat shock 70kD protein 9B (mortalin-2)
NIP71	U83843_at	U83843	fail	4		PASS	13	4	6.77	Normal	Normal	Nip7-1		HIV-1 Nef interacting protein	similar to murine CCT (chaperonin containing TCP-1) eta subunit encoded by GenBank Accession Number Z31399; CCT assists the folding of proteins in eukaryotic cytosol; Nef enhances the infectivity of HIV and SIV
APT1	D49396_at	D49396	fail	4		PASS	13	4	4.85	Normal	Normal			Aop1_Human, MER5(Aop1_Mouse)-like protein	
RAB1	M28209_at	M28209	fail	3		PASS	13	3	6.23	Normal	Normal	RAB1	2p14-p13.4	RAB1, member RAS oncogene family	RAB1, member RAS oncogene family
M28213_s_at	M28213_s_at	M28213	fail	3		PASS	13	3	5.77	Normal	Normal	RAB2		RAB2, member RAS oncogene family	RAB2, member RAS oncogene family
L00634_s_at	L00634_s_at	L00634	fail	2		PASS	13	2	6.15	Normal	Normal	FN1A	8p22-q11	farnesyltransferase, CAAX box, alpha	farnesyltransferase, CAAX box, alpha
PEPD	J04605_at	J04605	fail	2		PASS	13	2	5.38	Normal	Normal	PEPD	19q12-q13.2	peptidase D	peptidase D
SEC7PL	U59752_at	U59752	fail	4		PASS	12	4	7.92	Normal	Normal	PSCD2		pleckstrin homology, Sec7 and coiled/coiled domains 2 (cytohesin-2)	pleckstrin homology, Sec7 and coiled/coiled domains 2 (cytohesin-2)
K112	D25218_at	D25218	fail	4		PASS	12	4	6.42	Normal	Normal	KIAA0112		transcription elongation factor A (SII)-like 1	transcription elongation factor A (SII)-like 1
PP21	M99701_at	M99701	fail	4		PASS	12	4	5.75	Normal	Normal	TCEAL1	Xq22.1		
AFFX-BioB-AFFX-BioB-AFFX-BioB			fail	3		PASS	12	3	10.75	Normal	Normal	CREBBP	16p13.3	CREB binding protein (Rubinstein-Taybi syndrome)	CREB binding protein (Rubinstein-Taybi syndrome)
E_CREBBP	U89355_at	U89355	fail	3		PASS	12	3	5.17	Normal	Normal	CUL1		cullin 1	cullin 1
CUL1	U58087_at	U58087	fail	4		PASS	11	4	8.64	Normal	Normal	FACLI		long-chain acyl-CoA synthetase	ATP-binding domain (bp. 1447..1846)
L09229_s_at	L09229_s_at	L09229	fail	4		PASS	11	4	8.36	Normal	Normal			mitochondrial citrate transport protein	
SLC20A3_m	X96924_ma	X96924	fail	4		PASS	11	4	8.18	Normal	Normal				
K233_COST	D87071_at	D87071	fail	4		PASS	11	4	7.45	Normal	Normal	KIAA0233		KIAA0233 gene product	
E_23773	U90904_at	U90904	fail	4		PASS	11	4	7.00	Normal	Normal				
MTHFD	L38928_at	L38928	fail	4		PASS	11	4	6.73	Normal	Normal			5,10-methylenetetrahydrofolate synthetase	
MEF	U32645_at	U32645	fail	4		PASS	11	4	6.27	Normal	Normal	ELF4		E74-like factor 4 (ets domain transcription factor)	E74-like factor 4 (ets domain transcription factor)
OAT	M29927_at	M29927	fail	4		PASS	11	4	6.00	Normal	Normal	OAT	10q26	ornithine aminotransferase (gyrate atrophy)	ornithine aminotransferase (gyrate atrophy)
MPV17	X76538_at	X76538	fail	4		PASS	11	4	5.82	Normal	Normal	MPV17	2p23-p21	MpV17 transgene, murine homolog, glomerulosclerosis	MpV17 transgene, murine homolog, glomerulosclerosis
FH	U59309_at	U59309	fail	4		PASS	11	4	5.73	Normal	Normal	FH	1q42.1	fumarate hydratase	fumarate hydratase
GBP1	M55542_at	M55542	fail	4		PASS	11	4	5.64	Normal	Normal	GBP1	1	guanylate binding protein 1, interferon-inducible, 67kD	guanylate binding protein 1, interferon-inducible, 67kD
ARF6	M57763_at	M57763	fail	3		PASS	11	3	7.64	Normal	Normal	ARF6		ADP-ribosylation factor 6	ADP-ribosylation factor 6



GUBP	U78524_at	U78524	fail	3	PASS	11	3	6.00	Normal	Normal	DDXBP1	15q	DEAD/H (Asp-Glu-Ala-Asp/His) box binding protein 1	DEAD/H (Asp-Glu-Ala-Asp/His) box binding protein 1
E 23828	U79285_at	U79285	fail	3	PASS	11	3	5.73	Normal	Normal				
PTEN	U92436_at	U92436	fail	3	PASS	11	3	5.00	Normal	Normal	PTEN	10q23	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)
SLBP	U75679_at	U75679	fail	3	PASS	11	3	4.91	Normal	Normal	SLBP		histone stem-loop binding protein	
AFEX-HSAC	AFEX-HSAC	AFEX-HSAC	fail	1	PASS	11	1	7.27	Normal	Normal				
U04806 s at	U04806 s at	U04806	fail	4	PASS	10	4	8.90	Normal	Normal			FL13/FLK2 ligand	
TRIP7	L40357_at	L40357	fail	4	PASS	10	4	7.60	Normal	Normal	TRIP7		thyroid receptor interactor 7	thyroid hormone receptor interactor 7
STAT1	M97936_at	M97936	fail	4	PASS	10	4	7.50	Normal	Normal				
LRMP	U10485_at	U10485	fail	4	PASS	10	4	7.00	Normal	Normal	LRMP		lymphoid-restricted membrane protein	lymphoid-restricted membrane protein
LAP18_ma1	M31303_ma	M31303	fail	4	PASS	10	4	6.60	Normal	Normal	Op18		oncoprotein 18	
DIFF48	U49187_at	U49187	fail	4	PASS	10	4	6.50	Normal	Normal	DIFF48			
SNRPD3	U15009_at	U15009	fail	4	PASS	10	4	6.40	Normal	Normal	SNRPD3		small nuclear ribonucleoprotein D3 polypeptide (18kD)	small nuclear ribonucleoprotein D3 polypeptide (18kD)
X62153 s at	X62153 s at	X62153	fail	4	PASS	10	4	6.30	Normal	Normal			P11 protein	
CTR2	U83461_at	U83461	fail	4	PASS	10	4	6.20	Normal	Normal	SLC31A2	9q31-q32	solute carrier family 31 (copper transporters), member 2	solute carrier family 31 (copper transporters), member 2
GPCR	L42324_at	L42324	fail	4	PASS	10	4	6.10	Normal	Normal	GPCR		G protein-linked receptor	
EIF5	U49436_at	U49436	fail	4	PASS	10	4	6.00	Normal	Normal	EIF5		eukaryotic translation initiation factor 5	eukaryotic translation initiation factor 5
K100_EL	D43947_at	D43947	fail	4	PASS	10	4	5.90	Normal	Normal	KIAA0100		KIAA0100 gene product	KIAA0100 gene product
K274_HYON	D87464_at	D87464	fail	4	PASS	10	4	5.90	Normal	Normal	KIAA0274		glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)	glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)
GOT2	M22632_at	M22632	fail	4	PASS	10	4	5.90	Normal	Normal	GOT2	16q21	glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)	glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)
DGUOK	U41668_at	U41668	fail	4	PASS	10	4	5.90	Normal	Normal	DGUOK		deoxyguanosine kinase	deoxyguanosine kinase
IRRCF	U18321_at	U18321	fail	4	PASS	10	4	5.80	Normal	Normal	DAP3	1q21	Death associated protein 3	Death associated protein 3
HZF1	X78924_at	X78924	fail	4	PASS	10	4	5.80	Normal	Normal	HZF1		zinc finger protein	
D29640 s at	D29640 s at	D29640	fail	4	PASS	10	4	5.70	Normal	Normal	SAR1	15	rasGAP-like with IQ motifs	rasGAP-like with IQ motifs
SNRPA1	X13482_at	X13482	fail	4	PASS	10	4	5.60	Normal	Normal	SNRPA1		small nuclear ribonucleoprotein polypeptide A'	small nuclear ribonucleoprotein polypeptide A'
U47686 s at	U47686 s at	U47686	fail	4	PASS	10	4	5.10	Normal	Normal			signal transducer and activator of transcription Stat5B	STAT protein; is activated by IL-2, IL-7, IL-15, growth hormone, IL-3, GM-CSF, thrombopoietin, prolactin, and erythropoietin; tyrosine 699 phosphorylation is required for activation and dimerization of Stat5B
K267_NAHE	D87743_at	D87743	fail	4	PASS	10	4	4.80	Normal	Normal	KIAA0267		Similar to Human Na+/H+ exchanger 2 (A57644)	Similar to Human Na+/H+ exchanger 2 (A57644)
RPP38	U77664_at	U77664	fail	4	PASS	10	4	4.70	Normal	Normal	RPP38		RNAseP protein P38	RNAseP protein P38
L38593 s at	L38593 s at	L38593	fail	3	PASS	10	3	6.50	Normal	Normal	NRAMP1		integral membrane protein	alternative
TBI	M74089_at	M74089	fail	3	PASS	10	3	5.50	Normal	Normal	TBI		cholesterase-related cell division controller	cholesterase-related cell division controller
CHED	M80629_at	M80629	fail	3	PASS	10	3	5.30	Normal	Normal	CDC2L		cholesterase-related cell division controller	cholesterase-related cell division controller
RCPN	U03644_at	U03644	fail	3	PASS	10	3	5.30	Normal	Normal	CIR		CBF1 interacting corepressor	CBF1 interacting corepressor
CCNG2	U47414_at	U47414	fail	3	PASS	10	3	5.30	Normal	Normal	CCNG2		cyclin G2	cyclin G2
E 23721	U79291_at	U79291	fail	3	PASS	10	3	5.00	Normal	Normal				

L1VP	L13800 at M86852_at	fail	3		PASS	10	3	4.90	Normal	Normal	Normal	PXMP3	8q21.1	peroxisomal membrane protein 3 (35kD, Zellweger syndrome)	peroxisomal membrane protein 3 (35kD, Zellweger syndrome)
CPSPF	U37012_at	fail	4		PASS	9	4	8.00	Normal	Normal	Normal			cleavage and polyadenylation specificity factor	160 kDa subunit
CD9	M38690 at AF000177_at	fail	4		PASS	9	4	7.33	Normal	Normal	Normal	CD9	12p13	CD9 antigen (p24)	CD9 antigen (p24)
CASM	AF000177_at	fail	4		PASS	9	4	7.11	Normal	Normal	Normal	CaSm		Sm-like protein; encodes Sm motifs; overexpressed in pancreatic cancer	
K138 THH	D50928 at U03891_at	fail	4		PASS	9	4	7.00	Normal	Normal	Normal	KIAA0138		KIAA0138 gene product	
PHBLN1	U03891_at	fail	4		PASS	9	4	5.89	Normal	Normal	Normal	DJ742C19.2	22q12.3-q13.1	phorbolin (similar to apolipoprotein B mRNA editing protein)	phorbolin (similar to apolipoprotein B mRNA editing protein)
HLA-DPB1	M83664 at D87438_at	fail	4		PASS	9	4	5.67	Normal	Normal	Normal	HLA-DPB1		HLA-DPB1	Similar to a C.elegans protein in cosmid C14H10
K251_COSC	D87438_at	fail	4		PASS	9	4	5.44	Normal	Normal	Normal	KIAA0251		sorbinol dehydrogenase	sorbinol dehydrogenase
SORD	L29008 at D42054_at	fail	4		PASS	9	4	5.33	Normal	Normal	Normal	SORD	15q15-q21.1	replication protein A3 (14kD)	KIAA0092 gene product
K92_MYH6	D42054_at	fail	4		PASS	9	4	5.22	Normal	Normal	Normal	KIAA0092	7	sterol carrier protein 2	sterol carrier protein 2
RECA	L07493 at U11313_at	fail	4		PASS	9	4	4.89	Normal	Normal	Normal	RPA3		YY1-associated factor 2	YY1-associated factor 2
SCP2	U11313_at	fail	4		PASS	9	4	4.89	Normal	Normal	Normal	SCP2	1pter-p21	protein phosphatase 2 (formerly protein phosphatase 2A)	protein phosphatase 2 (formerly protein phosphatase 2A)
YAF2	U72209 at M65254_at	fail	4		PASS	9	4	4.78	Normal	Normal	Normal	YAF2	11q23	regulatory subunit-beta	regulatory subunit-beta
PPP2R1B	M65254_at	fail	4		PASS	9	4	4.56	Normal	Normal	Normal	PPP2R1B		killer cell lectin-like receptor subfamily D, member 1	killer cell lectin-like receptor subfamily D, member 1
CD94	U30610_at	fail	3		PASS	9	3	8.44	Normal	Normal	Normal	KLRD1	12p13	small nuclear ribonucleoprotein polypeptide B*	small nuclear ribonucleoprotein polypeptide B*
SNRNPB2	M15841_at	fail	3		PASS	9	3	7.44	Normal	Normal	Normal	SNRNPB2		Charot-Leyden crystal protein	Charot-Leyden crystal protein
CLC	L01664 at AF000177_at	fail	3		PASS	9	3	7.22	Normal	Normal	Normal	CLC	19q13.1	sorting nexin 1	sorting nexin 1
AF000177_at	AF000177_at	fail	3		PASS	9	3	7.11	Normal	Normal	Normal	SNX1		FK506-binding protein 5	FK506-binding protein 5
SNX1	U53225 at U42031_at	fail	3		PASS	9	3	6.67	Normal	Normal	Normal	SNX1		SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1
PKBP5	U42031_at	fail	3		PASS	9	3	6.56	Normal	Normal	Normal	PKBP5		MAP kinase kinase	MAP kinase kinase
S72024 s at S72024 s at	S72024 s at S72024 s at	fail	3		PASS	9	3	6.44	Normal	Normal	Normal	SMARCC1	3p23-p21	tripeptidyl peptidase II	tripeptidyl peptidase II
SMARCC1	U66615_at	fail	3		PASS	9	3	5.67	Normal	Normal	Normal	SMARCC1		pLK	pLK
														signal transducer and activator of transcription 6, interleukin-4 induced	signal transducer and activator of transcription 6, interleukin-4 induced
L05624 s at L05624 s at	L05624 s at L05624 s at	fail	3		PASS	9	3	5.56	Normal	Normal	Normal	TPP2	13q32-q33	nucleoporin 88kD	nucleoporin 88kD
TPP2	M73047 at U01038_at	fail	3		PASS	9	3	5.56	Normal	Normal	Normal	TPP2		propionyl Coenzyme A carboxylase, alpha polypeptide	propionyl Coenzyme A carboxylase, alpha polypeptide
PLK	U01038_at	fail	3		PASS	9	3	5.56	Normal	Normal	Normal	STAT6	12q13	induced	induced
STAT6	U16031_at	fail	3		PASS	9	3	5.56	Normal	Normal	Normal	STAT6		nucleoporin 88kD	nucleoporin 88kD
														propionyl Coenzyme A carboxylase, alpha polypeptide	propionyl Coenzyme A carboxylase, alpha polypeptide
NUP88	Y08612 at S79219 s at	fail	3		PASS	9	3	5.44	Normal	Normal	Normal	NUP88	17p13	propionyl Coenzyme A carboxylase, alpha polypeptide	propionyl Coenzyme A carboxylase, alpha polypeptide
S79219 s at	S79219 s at	fail	3		PASS	9	3	5.22	Normal	Normal	Normal	PCCA	13q32		

C2F	U72514_at	U72514	fail	3		PASS	9	3	5.00	Normal	Normal	C2F	C2F	similar to EST with GenBank Accession Number R64505; similar to S. cerevisiae hypothetical protein L9470.5 encoded by GenBank Accession Number S51431, and to S. pombe hypothetical 34.9 KD protein encoded by GenBank Accession Number Z68198; see corresponding genomic sequence in GenBank Accession Number U72506
E_23733	U79274_at	U79274	fail	3		PASS	9	3	5.00	Normal	Normal			deoxycytidine kinase
DCK	M60527_at	M60527	fail	3		PASS	9	3	4.67	Normal	Normal			deoxycytidine kinase
AFFX-BioB	AFFX-BioB	AFFX-BioB	fail	0		PASS	9	0	17.44	Normal	Normal			
RES424A	AB000464_at	AB000464	fail	4		PASS	8	4	8.50	Normal	Normal			structure specific recognition protein 1
SSRP1	M86737_at	M86737	fail	4		PASS	8	4	7.75	Normal	Normal			structure specific recognition protein 1
BAT3	M33521_at	M33521	fail	4		PASS	8	4	7.50	Normal	Normal			HLA-B associated transcript-3
PNOC	U48263_at	U48263	fail	4		PASS	8	4	7.00	Normal	Normal			pre-pro-orphanin FQ
ERCC1	M13194_at	M13194	fail	4		PASS	8	4	6.63	Normal	Normal			excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence)
TRNAGUTR	U30888_at	U30888	fail	4		PASS	8	4	6.38	Normal	Normal			ubiquitin specific protease 14 (RNA-guanine transglycosylase)
L24774_s_at	L24774_s_at	L24774	fail	4		PASS	8	4	5.88	Normal	Normal			dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)
HG3319-HT3	HG3319-HT3	HG3319-H	fail	4		PASS	8	4	5.63	Normal	Normal			neuraminidase
G9	X78687_at	X78687	fail	4		PASS	8	4	5.38	Normal	Normal			neuraminidase
ZNF139	U09848_at	U09848	fail	4		PASS	8	4	5.00	Normal	Normal			zinc finger protein 139 (clone pTZ-37)
ZFX	X59739_at	X59739	fail	4		PASS	8	4	5.00	Normal	Normal			zinc finger protein, X-linked
S80267_s_at	S80267_s_at	S80267	fail	4		PASS	8	4	4.88	Normal	Normal			This sequence comes from Fig. 3.
DARS	J05032_at	J05032	fail	4		PASS	8	4	4.63	Normal	Normal			aspartyl-tRNA synthetase
U18271_cds3	U18271_cds3	U18271	fail	4		PASS	8	4	4.63	Normal	Normal			thymopoietin beta
K128_HCDG	D50918_at	D50918	fail	3		PASS	8	3	7.13	Normal	Normal			The KIAA0128 gene is related to cdc10.
TDRKAA	HG3578-HT3	HG3578-H	fail	3		PASS	8	3	6.25	Normal	Normal			lamin B2
LAMB2	M94362_at	M94362	fail	3		PASS	8	3	6.00	Normal	Normal			GAP SH3 binding protein
SH3BP2	U32519_at	U32519	fail	3		PASS	8	3	5.50	Normal	Normal			
MURR1	D85433_at	D85433	fail	3		PASS	8	3	5.38	Normal	Normal			integrin, alpha E (antigen CD103, human mucosal lymphocyte antigen 1; alpha polypeptide)
ITGAE	L25851_at	L25851	fail	3		PASS	8	3	5.25	Normal	Normal			integrin, alpha E (antigen CD103, human mucosal lymphocyte antigen 1; alpha polypeptide)
SP1REGSUP	U08377_at	U08377	fail	3		PASS	8	3	5.25	Normal	Normal			splicing factor, arginine/serine-rich 8 (suppressor-of-white-apricot, Drosophila homolog)

STX16C	AF008937 at U37139_at	fail	3	PASS	8	3	5.00	Normal	Normal	STX16	synixin 16	synixin 16
ANXB3	U37139_at	fail	3	PASS	8	3	4.88	Normal	Normal		beta 3-endonoxin long form	The long form does not bind to the integrin beta 3 subunit cytoplasmic domain
K33	D26067 at D26067	fail	3	PASS	8	3	4.75	Normal	Normal	KIAA0033		
AHR	L19872 at L19872	fail	3	PASS	8	3	4.75	Normal	Normal	AHR	aryl hydrocarbon receptor	aryl hydrocarbon receptor
MEST	D78611 at D78611	fail	3	PASS	8	3	4.38	Normal	Normal	MEST	mesoderm specific transcript (mouse) homolog	mesoderm specific transcript (mouse) homolog
PIGH	L19783 at L19783	fail	3	PASS	8	3	4.38	Normal	Normal	PIGH	phosphatidylinositol glycan, class H	phosphatidylinositol glycan, class H
M34338 s at M34338	U96113 at U96113	fail	2	PASS	8	2	7.50	Normal	Normal	SRM	spermidine synthase	spermidine synthase
WWP1	U96113 at U96113	fail	2	PASS	8	2	5.88	Normal	Normal	WWP1	Nedd4-like ubiquitin-protein ligase; WW domain-containing protein	Nedd4-like ubiquitin-protein ligase; WW domain-containing protein
RH17599	L06175 at L06175	fail	2	PASS	8	2	5.75	Normal	Normal	P5-1		occurs in MHC class I region; ORF
ITBA1	X92475 at X92475	fail	2	PASS	8	2	5.75	Normal	Normal	ITBA1	ITBA1 protein	ITBA1 gene
CL1042	X70649 at X70649	fail	2	PASS	8	2	5.38	Normal	Normal	DDX1	member of DEAD box protein family	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1
HG3417-HT3	HG3417-HT3	fail	2	PASS	8	2	5.25	Normal	Normal		tactile protein	T cell surface antigen, increased during activation'
TACT	M88282 at M88282	fail	2	PASS	8	2	5.25	Normal	Normal			
ZFP2	U71598 at U71598	fail	2	PASS	8	2	5.25	Normal	Normal	zfp2	zinc finger protein zfp2	
KL16 75KD	D29958 at D29958	fail	2	PASS	8	2	5.13	Normal	Normal	KIAA0116		
IMOG38	Z68747 at Z68747	fail	2	PASS	8	2	5.13	Normal	Normal		inogen 38	proprotein
BTG3	D64110 at D64110	fail	2	PASS	8	2	5.00	Normal	Normal		ANA	
RATC10	HG1879-HT3	fail	2	PASS	8	2	5.00	Normal	Normal			
GCF	M29204 at M29204	fail	2	PASS	8	2	5.00	Normal	Normal	TCF9	transcription factor 9 (binds GC-rich sequences)	transcription factor 9 (binds GC-rich sequences)
HG3546-HT3	HG3546-HT3	fail	2	PASS	8	2	4.88	Normal	Normal			
ATF1	X55544 at X55544	fail	2	PASS	8	2	4.75	Normal	Normal	ATF1	TREB protein	activating transcription factor 1
UNKP	U50950 at U50950	fail	2	PASS	8	2	4.13	Normal	Normal			
ALDOC	X05196 at X05196	fail	1	PASS	8	1	7.00	Normal	Normal	ALDOC	aldolase C	aldolase C, fructose-bisphosphate
SFC23B	X97065 at X97065	fail	1	PASS	8	1	6.13	Normal	Normal	sec23	Sec23 protein	COP1 component; isoform B
GTF2B	M76766 at M76766	fail	1	PASS	8	1	5.88	Normal	Normal	GTF2B	general transcription factor IIB	general transcription factor IIB
RPP30	U77665 at U77665	fail	1	PASS	8	1	5.63	Normal	Normal	RPP30	RNAseP protein P30	
COASYNT	Z68204 at Z68204	fail	1	PASS	8	1	5.50	Normal	Normal	SUCLG1	succinyl coenzyme A synthetase	succinate-CoA ligase, GDP-forming, alpha subunit
DDX3	U50553 at U50553	fail	1	PASS	8	1	5.13	Normal	Normal	DDX3	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3
SPR2	HG3088-HT3	fail	1	PASS	8	1	4.75	Normal	Normal			
CDIC	M28827 at M28827	fail	1	PASS	8	1	4.75	Normal	Normal	CDIC	CDIC antigen, c polypeptide	CDIC antigen, c polypeptide
BT2	M95809 at M95809	fail	1	PASS	8	1	4.75	Normal	Normal	BT2	basic transcription factor 62kD subunit	
TSNAX	X95073 at X95073	fail	1	PASS	8	1	4.75	Normal	Normal	TRAX	Translin associated protein X	
CSNK1A1	L37042 at L37042	fail	4	PASS	7	4	8.00	Normal	Normal	CSNK1A1	casein kinase 1, alpha 1	casein kinase 1, alpha 1
PLCD1	U09117 at U09117	fail	4	PASS	7	4	7.57	Normal	Normal		phospholipase c delta 1	
S10	D14889 at D14889	fail	4	PASS	7	4	5.71	Normal	Normal	RAB33A	RAB33A, member RAS oncogene family	RAB33A, member RAS oncogene family
AEBP1	D86479 at D86479	fail	4	PASS	7	4	5.71	Normal	Normal	AEBP1	AE-binding protein 1	AE-binding protein 1
SKB1	AF015913 at AF015913	fail	4	PASS	7	4	5.57	Normal	Normal	SKB1Hs	homolog of fission yeast Skb1	homolog of fission yeast Skb1



GTBP	U73737_at	U73737	fail	2		PASS	7	2	4.86	Normal	Normal	GTBP	2p16	G/T mismatch-binding protein	G/T mismatch-binding protein
U67932_s at	U67932		fail	2		PASS	7	2	4.57	Normal	Normal	cAMP phosphodiesterase			
GBE1	LO7956_at	LO7956	fail	2		PASS	7	2	4.43	Normal	Normal	glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type IV)	3p21	glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type IV)	glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type IV)
CDR2	M63256_at	M63256	fail	2		PASS	7	2	4.43	Normal	Normal	major Yo paraneoplastic antigen	16p13.1-p12	cerebellar degeneration-related protein (62kD)	cerebellar degeneration-related protein (62kD)
RPIH	U90437_at	U90437	fail	2		PASS	7	2	4.29	Normal	Normal				
HNRPA0	U23803_at	U23803	fail	1		PASS	7	1	8.71	Normal	Normal	heterogeneous ribonucleoprotein A0		hnRNP protein, hnRNA binding protein	hnRNP protein, hnRNA binding protein
ICRF	Z69915_at	Z69915	fail	1		PASS	7	1	6.00	Normal	Normal				
SSR1	Z12830_at	Z12830	fail	1		PASS	7	1	5.86	Normal	Normal	signal sequence receptor, alpha (translocon-associated protein alpha)		signal sequence receptor, alpha (translocon-associated protein alpha)	signal sequence receptor, alpha (translocon-associated protein alpha)
RALGDS	U14417_at	U14417	fail	1		PASS	7	1	5.71	Normal	Normal	Ral guanine nucleotide dissociation stimulator		the C-terminal non-catalytic domain of the Ral GDS interacts with Ras	the C-terminal non-catalytic domain of the Ral GDS interacts with Ras
SMARCC2	U66616_at	U66616	fail	1		PASS	7	1	5.71	Normal	Normal	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2	12q13-q14	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2
PCCB	S67325_at	S67325	fail	1		PASS	7	1	5.29	Normal	Normal	propionyl Coenzyme A carboxylase, beta polypeptide	3q21-q22	propionyl Coenzyme A carboxylase, beta polypeptide	propionyl Coenzyme A carboxylase, beta polypeptide
G16P	U50839_at	U50839	fail	1		PASS	7	1	5.00	Normal	Normal	g16 protein		g16 protein	g16 protein
CUL2	U83410_at	U83410	fail	1		PASS	7	1	5.00	Normal	Normal	cullin 2		cullin 2	cullin 2
CEBPG	U20240_at	U20240	fail	1		PASS	7	1	4.86	Normal	Normal	CCAAT/enhancer binding protein (C/EBP), gamma		CCAAT/enhancer binding protein (C/EBP), gamma	CCAAT/enhancer binding protein (C/EBP), gamma
RAB9	U44103_at	U44103	fail	1		PASS	7	1	4.86	Normal	Normal	RAB9, member RAS oncogene family		RAB9, member RAS oncogene family	RAB9, member RAS oncogene family
K55 TRE	D29956_at	D29956	fail	1		PASS	7	1	4.43	Normal	Normal	ubiquitin specific protease 8		ubiquitin specific protease 8	ubiquitin specific protease 8
CRIP2	D42123_at	D42123	PASS	9	25.56	fail	5	9		Disease	Disease	cysteine-rich protein 2	14q32.3	cysteine-rich protein 2	cysteine-rich protein 2
K14	D25216_at	D25216	PASS	9	31.67	fail	5	9		Disease	Disease	KIAA0014 gene product		KIAA0014 gene product	KIAA0014 gene product
LTK	D16105_at	D16105	PASS	9	23.78	fail	3	9		Disease	Disease	leukocyte tyrosine kinase	15	leukocyte tyrosine kinase	leukocyte tyrosine kinase
K60 GNPTA	D31766_at	D31766	PASS	8	14.50	fail	6	8		Disease	Disease	KIAA0060		KIAA0060 gene product	KIAA0060 gene product
CDK2	M68520_at	M68520	PASS	8	7.63	fail	6	8		Disease	Disease	cyclin-dependent kinase 2	12q13	cyclin-dependent kinase 2	cyclin-dependent kinase 2
IL11RA	U32324_at	U32324	PASS	8	9.75	fail	6	8		Disease	Disease	interleukin 11 receptor, alpha	9p13	interleukin 11 receptor, alpha	interleukin 11 receptor, alpha
ACP2_mal	X15525_mal	X15525	PASS	8	8.75	fail	6	8		Disease	Disease	acid phosphatase		acid phosphatase	acid phosphatase
H326	U06631_at	U06631	PASS	8	23.13	fail	5	8		Disease	Disease			homologous to mouse gene PC326;GenBank Accession Number M95564	homologous to mouse gene PC326;GenBank Accession Number M95564
TEB4	AF009301_at	AF009301	PASS	8	9.88	fail	5	8		Disease	Disease	TEB4 protein		TEB4 protein	TEB4 protein
K170_CALT	D79992_at	D79992	PASS	8	6.88	fail	5	8		Disease	Disease	KIAA0170		KIAA0170 gene product	KIAA0170 gene product
PRKACG	M34182_at	M34182	PASS	8	41.00	fail	5	8		Disease	Disease	protein kinase, cAMP-dependent, catalytic, gamma	9q13	protein kinase, cAMP-dependent, catalytic, gamma	protein kinase, cAMP-dependent, catalytic, gamma
PLEC1	U53204_at	U53204	PASS	8	40.38	fail	4	8		Disease	Disease	plectin 1, intermediate filament binding protein, 500kD	8q24	plectin 1, intermediate filament binding protein, 500kD	plectin 1, intermediate filament binding protein, 500kD
E_LF113	U18009_at	U18009	PASS	8	13.00	fail	4	8		Disease	Disease			similar to Pacific ray VAT1 protein, Swiss-Prot Accession Number P19333	similar to Pacific ray VAT1 protein, Swiss-Prot Accession Number P19333
18SRNA5	AFFX-HUM1	AFFX-HUM1	PASS	8	12.00	fail	3	8		Disease	Disease				
MUC3	HG2147-HT2	HG2147-H	PASS	8	60.63	fail	3	8		Disease	Disease				

MYBPC3	X73113_at	X73113	PASS	8	11.25	fail	3	8	Disease	Disease	MYBPC2	19	myosin-binding protein C, fast-type
NB	D89016_at	D89016	PASS	8	20.63	fail	2	8	Disease	Disease	nbr		myosin-binding protein C, fast-type
U47025_s_at	U47025_s_at	U47025	PASS	7	27.43	fail	6	7	Disease	Disease	PYGB	20	phosphorylase, glycogen; brain
KIDNABP	D45132_at	D45132	PASS	7	5.86	fail	6	7	Disease	Disease			zinc-finger DNA-binding protein
K179_HYPD	D80001_at	D80001	PASS	7	8.00	fail	6	7	Disease	Disease	KIAA0179		similar to hypothetical protein D4478 of S.cerevisiae
K213	D86968_at	D86968	PASS	7	4.14	fail	6	7	Disease	Disease	KIAA0213		Similar to Mouse TfIIi-associated transactivator factor p17(GB, RO,MMU11548)
HG2175-HT2	HG2175-HT2	HG2175-H	PASS	7	5.43	fail	6	7	Disease	Disease			Containing protein kinase motif
INPL1	L36818_at	L36818	PASS	7	21.71	fail	6	7	Disease	Disease			
GSI	M86934_at	M86934	PASS	7	8.14	fail	6	7	Disease	Disease	GSI		Gene from Xp22.3 which escapes X-inactivation. Function unknown.
MFAP1	U04209_at	U04209	PASS	7	6.00	fail	6	7	Disease	Disease			
IFNRG7A	U53830_at	U53830	PASS	7	15.29	fail	6	7	Disease	Disease	IRF7	11	associated microfilillar interferon regulatory factor 7
GABRA1	X14766_at	X14766	PASS	7	8.71	fail	6	7	Disease	Disease	GABRA1	5q34-q35	gamma-aminobutyric acid (GABA)
CSRP1	M76378_at	M76378	PASS	7	23.29	fail	5	7	Disease	Disease	CSRP1	1q32	(GABA) A receptor, alpha 1
K146	D63480_at	D63480	PASS	7	6.14	fail	5	7	Disease	Disease	KIAA0146		cysteine and glycine-rich protein 1
GLGF2	HG4704-HT2	HG4704-H	PASS	7	6.14	fail	5	7	Disease	Disease			The KIAA0146 gene product is novel
TAL1	M63589_at	M63589	PASS	7	13.00	fail	5	7	Disease	Disease	TAL1	1p32	T-cell acute lymphocytic leukemia 1
SLAHBP1	U51586_at	U51586	PASS	7	8.29	fail	5	7	Disease	Disease	SLAHBP1		sial binding protein 1
ENO2_ma1	X51956_ma1	X51956	PASS	7	9.43	fail	5	7	Disease	Disease	ENO2	12p13	human gamma enolase
K27	D25217_at	D25217	PASS	7	16.29	fail	4	7	Disease	Disease	KIAA0027		enolase 2, (gamma, neuronal)
EBI3	L08187_at	L08187	PASS	7	13.86	fail	4	7	Disease	Disease	EBI3		
RETROTP	Z48633_at	Z48633	PASS	7	12.14	fail	4	7	Disease	Disease			cytokine receptor
SP2	D28588_at	D28588	PASS	6	6.83	fail	6	6	Disease	Disease	SP2		
K263_HYPY	D87452_at	D87452	PASS	6	13.33	fail	6	6	Disease	Disease	KIAA0263		Sp2 transcription factor
HEPG2	K03195_at	K03195	PASS	6	9.50	fail	6	6	Disease	Disease	SGLT1		KIAA0263 gene product
IDS	L40586_at	L40586	PASS	6	6.67	fail	6	6	Disease	Disease	IDS	Xq27.3-q28	glucose transporter glycoprotein
FOSB	L49169_at	L49169	PASS	6	10.67	fail	6	6	Disease	Disease	GOS3		iduronate 2-sulfatase (Hunter syndrome)
MYOIC	U14391_at	U14391	PASS	6	9.00	fail	6	6	Disease	Disease	MYOIC	15q21-q22	GOS3 is human homolog of mouse FOSB gene
HCCS	U36787_at	U36787	PASS	6	7.00	fail	6	6	Disease	Disease			myosin IC
HA2	X90761_at	X90761	PASS	6	8.67	fail	6	6	Disease	Disease	KRTHA2	17q12-q21	holocytochrome c-type synthetase
X92493_s_at	X92493_s_at	X92493	PASS	6	5.00	fail	6	6	Disease	Disease	PIP5K1B	9q13	keratin, hair, acidic.2
XPA	D14533_at	D14533	PASS	6	4.50	fail	5	6	Disease	Disease	XPA	9	phosphatidylinositol-4-phosphate 5-kinase, type 1, beta
K76	D38548_at	D38548	PASS	6	16.33	fail	5	6	Disease	Disease	KIAA0076		xeroderma pigmentosum, complementation group A
K268_C219F	D87742_at	D87742	PASS	6	5.17	fail	5	6	Disease	Disease	KIAA0268		KIAA0076 gene product
DAO	HG2280-HT2	HG2280-H	PASS	6	15.50	fail	5	6	Disease	Disease			Similar to Human C219-reactive peptide (1.34688)

H2A1B	L19778_at	L19778	PASS	6	5.00	fail	5	6	Disease	Disease	H2APP	3p21	histone H2A.1b	H2A histone family, member P
MAP4	M64571_at	M64571	PASS	6	11.83	fail	5	6	Disease	Disease	MAP4		microtubule-associated protein 4	microtubule-associated protein 4
PML	M79462_at	M79462	PASS	6	12.00	fail	5	6	Disease	Disease	PML	15q22	promyelocytic leukemia	promyelocytic leukemia
S78798_s_at	S78798_s_at	S78798	PASS	6	6.50	fail	5	6	Disease	Disease	1-phosphatidylinositol-4-phosphate 5-kinase isoform C, PtdIns4P 5-kinase isoform C		Method: conceptual translation with partial peptide sequencing. This sequence comes from Fig. 2; PtdIns4P 5-kinase isoform C	
HSD17B3	U05659_at	U05659	PASS	6	18.17	fail	5	6	Disease	Disease	HSD17B3	9q22	hydroxysteroid (17-beta) dehydrogenase 3	hydroxysteroid (17-beta) dehydrogenase 3
ASMT	U11090_at	U11090	PASS	6	11.50	fail	5	6	Disease	Disease	ASMT	Xpter-p22.32 and Yp11.3	acetylserotonin N-methyltransferase	acetylserotonin N-methyltransferase
MHC2TA	U18259_at	U18259	PASS	6	5.00	fail	5	6	Disease	Disease	MHC2TA	Chr.16	MHC class II transactivator	MHC class II transactivator
U22431_s_at	U22431_s_at	U22431	PASS	6	6.83	fail	5	6	Disease	Disease	HIF1A	14q21-q24	hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)
SNAP	U39412_at	U39412	PASS	6	16.50	fail	5	6	Disease	Disease	NAPA		N-ethylmaleimide-sensitive factor attachment protein, alpha	N-ethylmaleimide-sensitive factor attachment protein, alpha
U43189_s_at	U43189_s_at	U43189	PASS	6	7.17	fail	5	6	Disease	Disease	NERF-1a,b		NERF-1b	Ets transcription factor
CHM	U84720_at	U84720	PASS	6	11.83	fail	5	6	Disease	Disease	RAE1;		Homolog of yeast Rae1 (Bharathi) mRNA-associated protein of 41 kDa (Kraemer)	homolog of yeast Rae1 (Bharathi) mRNA-associated protein of 41 kDa (Kraemer)
ITGA6	X53586_ma1	X53586	PASS	6	8.83	fail	5	6	Disease	Disease	ITGA6	2	integrin, alpha 6	integrin, alpha 6
LY64	D83597_at	D83597	PASS	6	11.83	fail	4	6	Disease	Disease	LY64	5q12	lymphocyte antigen 64 (mouse) homolog, radioprotective, 105kD	lymphocyte antigen 64 (mouse) homolog, radioprotective, 105kD
MLLT3	L13744_at	L13744	PASS	6	5.00	fail	4	6	Disease	Disease	AF-9		karyopherin alpha 1 (importin alpha 5)	karyopherin alpha 1 (importin alpha 5)
KPNA1	S75295_at	S75295	PASS	6	5.67	fail	4	6	Disease	Disease	KPNA1		zinc finger protein 169	zinc finger protein 169
ZNF133	U09366_at	U09366	PASS	6	7.50	fail	4	6	Disease	Disease	ZNF169	9q22	N-sulfoglucosamine sulfolactase (sulfamidase)	N-sulfoglucosamine sulfolactase (sulfamidase)
SGSH	U30894_at	U30894	PASS	6	10.50	fail	4	6	Disease	Disease	SGSH	17q25.3	aminomethyltransferase (glycine cleavage system protein T)	aminomethyltransferase (glycine cleavage system protein T)
AMT	D14686_at	D14686	PASS	5	12.20	fail	6	5	Disease	Disease	AMT	3p21.2-p21.1	tumor necrosis factor (ligand) superfamily, member 6	tumor necrosis factor (ligand) superfamily, member 6
APT1LG1	D38122_at	D38122	PASS	5	5.40	fail	6	5	Disease	Disease	TNFSF6	1q23	DNA2 (DNA replication helicase, yeast, homolog)-like	DNA2 (DNA replication helicase, yeast, homolog)-like
K83_CHR3	D42046_at	D42046	PASS	5	6.60	fail	6	5	Disease	Disease	DNA2L	10q21.3-q22.1	testis-specific kinase 1	testis-specific kinase 1
TESK1	D50863_at	D50863	PASS	5	8.80	fail	6	5	Disease	Disease	TESK1	9p13	similar to ankryrin of Chromatium vinosum.	similar to ankryrin of Chromatium vinosum.
K172_ANK3	D79994_at	D79994	PASS	5	6.20	fail	6	5	Disease	Disease	KIAA0172			
HG1783-HT	HG1783-HT	HG1783-HT	PASS	5	4.60	fail	6	5	Disease	Disease				
HGX12	HG2810-HT2	HG2810-HT2	PASS	5	6.00	fail	6	5	Disease	Disease				
X104	L27476_at	L27476	PASS	5	5.20	fail	6	5	Disease	Disease	ZO-2	9q13-q21	Friedreich ataxia region gene X104 (tight junction protein ZO-2)	Friedreich ataxia region gene X104 (tight junction protein ZO-2)



BRE	L38616_at	L38616	PASS	5	11.00	fail	6	5	Disease	Disease	BRE	brain and reproductive organ-expressed (TNFRSF1A modulator)	brain and reproductive organ-expressed (TNFRSF1A modulator)
ZNF8	M29581_at	M29581	PASS	5	8.80	fail	6	5	Disease	Disease	ZNF8	20q13	zinc finger protein 8 (clone HF-18)
U50648_s_at	U50648_s_at	U50648	PASS	5	24.60	fail	6	5	Disease	Disease	PRKR	2p22-p21	protein kinase, interferon-inducible double stranded RNA dependent
SCA2	U70323_at	U70323	PASS	5	12.20	fail	6	5	Disease	Disease	SCA2	12q24	ataxin 2
ADARB1	U76421_at	U76421	PASS	5	6.20	fail	6	5	Disease	Disease	ADARB1	21q22.3	adenosine deaminase, RNA-specific, B1 (homolog of rat RED1)
TSG101	U82130_at	U82130	PASS	5	7.80	fail	6	5	Disease	Disease	TSG101	22q13	tumor susceptibility protein
PMM1	U86070_at	U86070	PASS	5	12.60	fail	6	5	Disease	Disease	PMM1	22q13	phosphomannomutase 1
TST	X59434_at	X59434	PASS	5	8.80	fail	6	5	Disease	Disease	TST	10p15	thiosulfate sulfurtransferase (rhodanese)
PFKP	D25328_at	D25328	PASS	5	8.60	fail	5	5	Disease	Disease	PFKP	10p15	platelet-type phosphofructokinase, platelet
K65_ZNF11E	D31763_at	D31763	PASS	5	7.60	fail	5	5	Disease	Disease	KIAA0065		ha0946 protein is Kruppel-related
K188_SMP2	D80010_at	D80010	PASS	5	5.40	fail	5	5	Disease	Disease	KIAA0188		
HG2809-HT2	HG2809-HT2	HG2809-H	PASS	5	9.80	fail	5	5	Disease	Disease	ASGR2	17p	asialoglycoprotein receptor 2
M11025_s_at	M11025_s_at	M11025	PASS	5	6.40	fail	5	5	Disease	Disease	TPM1	15q22.1	tropomyosin 1 (alpha)
M19267_s_at	M19267_s_at	M19267	PASS	5	7.80	fail	5	5	Disease	Disease	TnC		putative slow twitch skeletal/cardiac muscle troponin C
TNNC1_ma	M37984_ma	M37984	PASS	5	12.80	fail	5	5	Disease	Disease	orf1_5' to PD-ECGF/TP		
ECGF1	S72487_at	S72487	PASS	5	10.00	fail	5	5	Disease	Disease	EIF2B5		eukaryotic translation initiation factor 2B, subunit 5 (epsilon, 82kD)
EIF2B	U23028_at	U23028	PASS	5	8.20	fail	5	5	Disease	Disease	CBLB	3q	Cas-Br-M (murine) ectropic retroviral transforming sequence b
CBLB	U26710_at	U26710	PASS	5	6.20	fail	5	5	Disease	Disease	ADK		putative polymerase; orf similar to the integrase domain of Type A and Type B retroviruses and to class II HERVs
ADK	U50196_at	U50196	PASS	5	5.00	fail	5	5	Disease	Disease	ERVK_cds2		alternative initiation codon used POU domain, class 2, associating factor 1
U68162_cds	U68162_cds	U68162	PASS	5	6.40	fail	5	5	Disease	Disease	U60269_cds2	11q23.1	clock (mouse) homolog similar to Mouse yolk sac permease like molecule 1 (U25739)
POU2AF1	Z49194_at	Z49194	PASS	5	7.20	fail	5	5	Disease	Disease	U60269_cds2	4q12	
K334	AB002332_at	AB002332	PASS	5	4.80	fail	4	5	Disease	Disease	KIAA0238		
K238_PERM	D87075_at	D87075	PASS	5	6.00	fail	4	5	Disease	Disease	KIAA0258	chr. 1	KIAA0258 gene product
K258	D87447_at	D87447	PASS	5	9.20	fail	4	5	Disease	Disease	EGFL2	1p21	EGF-like-domain, multiple 2
K279_EGFL	D87469_at	D87469	PASS	5	5.80	fail	4	5	Disease	Disease	AMY2B		amylase, alpha 2B; pancreatic
AMY2B	D90097_at	D90097	PASS	5	5.60	fail	4	5	Disease	Disease	M34458_ma		lamin B
M34458_ma	M34458_ma	M34458	PASS	5	5.80	fail	4	5	Disease	Disease			

M81182_s_a	M81182_s_a	M81182	PASS	5	5.00	fail	4	5		Disease	Disease	PXMP1	1p22-p21	peroxisomal membrane protein 1 (70kD, Zellweger syndrome)	peroxisomal membrane protein 1 (70kD, Zellweger syndrome)
HRC1	M91083_at	M91083	PASS	5	8.00	fail	4	5		Disease	Disease	C11ORF13	11p15.5	HRAS1-related cluster-1	chromosome 11 open reading frame 13
ITGB3	S70348_at	S70348	PASS	5	7.00	fail	4	5		Disease	Disease	integrin beta 3		integrin beta 3	This sequence comes from Fig. 1a. Protein sequence is in conflict with the conceptual translation; mismatch(29[G->G;Q])
PTFD	U44755_at	U44755	PASS	5	9.00	fail	4	5		Disease	Disease	SNAPC2		small nuclear RNA activating complex, polypeptide 2, 45kD	small nuclear RNA activating complex, polypeptide 2, 45kD
GCDH	U69141_at	U69141	PASS	5	6.40	fail	4	5		Disease	Disease	GCDH	19p13.2	glutaryl-Coenzyme A dehydrogenase	glutaryl-Coenzyme A dehydrogenase
UNKP	D28124_at	D28124	PASS	5	16.40	fail	3	5		Disease	Disease	NBL1	1p36.3-p36.2	neuroblastoma candidate region, suppression of tumorigenicity 1	neuroblastoma candidate region, suppression of tumorigenicity 1
NCBPI1	D59253_at	D59253	PASS	5	5.80	fail	3	5		Disease	Disease			NCBP Interacting Protein 1	RNA-binding protein that has two RNP consensus motifs
ITGB3	HG2320-HT2	HG2320-HT2	PASS	5	11.60	fail	3	5		Disease	Disease				
M33684_s_a	M33684_s_a	M33684	PASS	5	6.60	fail	3	5		Disease	Disease	PTPN1		non-receptor tyrosine phosphatase 1	
MYH10_r	U34301_r	U34301	PASS	5	15.40	fail	3	5		Disease	Disease				
X07438_s	X07438_s	X07438	PASS	5	9.00	fail	3	5		Disease	Disease				
CREB1	X68994_at	X68994	PASS	5	5.60	fail	3	5		Disease	Disease	CREB		Y protein	
MYL2	J02854_at	J02854	PASS	5	26.00	fail	2	5		Disease	Disease	MYL2		myosin light chain 2	
AC1	D82070_at	D82070	PASS	5	5.00	fail	2	5		Disease	Disease	ac1			
CGM7	D90276_at	D90276	PASS	5	14.60	fail	2	5		Disease	Disease	CGM7	19q13.2	carcinoembryonic antigen gene family member 7	carcinoembryonic antigen gene family member 7
HG4020-HT4	HG4020-HT4	HG4020-HT4	PASS	5	16.00	fail	2	5		Disease	Disease				
PKC1	L05144_at	L05144	PASS	5	5.60	fail	2	5		Disease	Disease	PKC1	20q13.31	phosphoenolpyruvate carboxykinase 1 (soluble)	phosphoenolpyruvate carboxykinase 1 (soluble)
DEFA5_ma1	M97925_ma1	M97925	PASS	5	9.00	fail	2	5		Disease	Disease	DEFA5	8pter-p21	defensin 5	defensin, alpha 5, Paneth cell-specific
CCNG1IP	U61836_at	U61836	PASS	5	8.80	fail	2	5		Disease	Disease				
KRT3	X82634_at	X82634	PASS	5	6.40	fail	2	5		Disease	Disease	KRT3A7	17q12-q21	keratin, hair, acidic, 7	keratin, hair, acidic, 7
NMOR2	J02888_at	J02888	PASS	7	12.71	PASS	8	7	6.38	1.99	1.99	NMOR2	6pter-q12	NAD(P)H menadiene oxidoreductase 2, dioxin-inducible	NAD(P)H menadiene oxidoreductase 2, dioxin-inducible
HG33-HT33	HG33-HT33	HG33-HT33	PASS	9	309.00	PASS	13	9	155.08	1.99	1.99				
RES422B	AB000460_a	AB000460	PASS	9	27.56	PASS	12	9	13.83	1.99	1.99	RES4-22	4p16.3	gene with multiple splice variants near HD locus on 4p16.3	gene with multiple splice variants near HD locus on 4p16.3
MIC2	M16279_at	M16279	PASS	9	72.22	PASS	13	9	36.31	1.99	1.99	MIC2	Xp22.32; Yp11.3	antigen identified by monoclonal antibodies 12E7, F21 and O13	antigen identified by monoclonal antibodies 12E7, F21 and O13
RB1	L22342_at	L22342	PASS	9	27.33	PASS	12	9	13.75	1.99	1.99	IF175		interferon-induced protein 75, 52kD	interferon-induced protein 75, 52kD
HLA-DNA	M31525_at	M31525	PASS	6	13.50	PASS	10	6	6.80	1.99	1.99	HLA-DNA		MHC HLA-DNA precursor	MHC HLA-DNA precursor
LRP1	X79882_at	X79882	PASS	7	27.29	PASS	12	7	13.75	1.98	1.98	LRP		lung resistance-related protein	lung resistance-related protein
RAGE_cds3	U89336_cds3	U89336	PASS	9	12.56	PASS	12	9	6.33	1.98	1.98	HBX2		homeobox PBX2 gene	intron-exon boundaries identified by a contig of ESTs with GenBank Accession Numbers W76064, R59617, W72507

J03805_s_at	J03805_s_at	J03805	PASS	9	14.33	PASS	13	9	7.23	1.98	1.98	8p12-p11.2	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform
ATOX1	U70660_at	U70660	PASS	8	13.38	PASS	12	8	6.75	1.98	1.98	5q32-q33	ATX1 (antioxidant protein 1, yeast) homolog 1	ATX1 (antioxidant protein 1, yeast) homolog 1
K22	D14664_at	D14664	PASS	8	16.50	PASS	12	8	8.33	1.98	1.98		KIAA0022	KIAA0022 gene product
SMS	Z49099_at	Z49099	PASS	9	20.44	PASS	12	9	10.33	1.98	1.98	Xp22.1	SMS	Spermine synthase
TCTEL1	D50663_at	D50663	PASS	8	22.75	PASS	12	8	11.50	1.98	1.98		TCTEL1	similar to murine Tctel1 gene product
CSTF3	U15782_at	U15782	PASS	8	11.38	PASS	12	8	5.75	1.98	1.98		CSTF3	cleavage stimulation factor, 3' pre-RNA, subunit 3, 77KD
PL1	M11119_at	M11119	PASS	7	15.00	PASS	12	7	7.58	1.98	1.98			pseudo-env cds/pseudo
M20867_s_a	M20867_s_a	M20867	PASS	8	14.13	PASS	13	8	7.15	1.97	1.97		GLUD1	glutamate dehydrogenase precursor (EC 1.4.1.3.)
G6PD	M24470_at	M24470	PASS	9	15.78	PASS	11	9	8.00	1.97	1.97	6p23	GNMPR	guanosine monophosphate reductase
K24_PTDS	D14694_at	D14694	PASS	9	41.11	PASS	13	9	20.85	1.97	1.97		KIAA0024	KIAA0024 gene product
REQ	U94585_at	U94585	PASS	9	19.11	PASS	13	9	9.69	1.97	1.97		hsReq	zinc finger; contains one C2H2 and two C4HC3
L19493_s_at	L19493_s_at	L19493	PASS	7	9.86	PASS	11	7	5.00	1.97	1.97		FMRI	
M12959_s_a	M12959_s_a	M12959	PASS	9	13.722	PASS	13	9	69.62	1.97	1.97		TCRA	T-cell receptor alpha-chain (VDIC)
TRSP	M86752_at	M86752	PASS	8	16.13	PASS	11	8	8.18	1.97	1.97		IEF SSP 3521	transformation-sensitive protein
MYCBP	D89667_at	D89667	PASS	9	114.11	PASS	13	9	57.92	1.97	1.97		PFDN5	prefoldin 5
MYL6	HG2815-HT	HG2815-H	PASS	9	292.33	PASS	13	9	148.46	1.97	1.97			
GOK	U52426_at	U52426	PASS	7	14.00	PASS	9	7	7.11	1.97	1.97	11p15.5	STIM1	stromal interaction molecule 1
ALDH7	U94252_at	U94252	PASS	8	13.63	PASS	13	8	6.92	1.97	1.97	1q22-q23	ALDH9	aldehyde dehydrogenase 9 (gamma-aminobutyraldehyde dehydrogenase, E3 isozyme)
ETFB	X71129_at	X71129	PASS	9	12.00	PASS	10	9	6.10	1.97	1.97	19q13.3	ETFB	electron-transfer-flavoprotein, beta polypeptide
DIPA	U63825_at	U63825	PASS	8	21.63	PASS	13	8	11.00	1.97	1.97		dipA	isolated in a two hybrid screen to identify cellular proteins that interact with hepatitis delta antigen; similar to hepatitis delta antigen, and has two regions predicted to form coiled-coil protein interaction domains
NAGA	M62783_at	M62783	PASS	9	16.44	PASS	13	9	8.38	1.96	1.96	22q13-qter	NAGA	N-acetylgalactosaminidase, alpha-
K317	AB002315_a	AB002315	PASS	9	11.11	PASS	12	9	5.67	1.96	1.96		KIAA0317	KIAA0317 gene product
GLB1	M34423_at	M34423	PASS	9	17.11	PASS	11	9	8.73	1.96	1.96	3p21.33	GLB1	galactosidase, beta 1
CDC34	L22005_at	L22005	PASS	6	12.00	PASS	8	6	6.13	1.96	1.96	19p13.3	CDC34	cell division cycle 34
AGC1	U16306_at	U16306	PASS	9	104.11	PASS	13	9	53.15	1.96	1.96			
SNRPN	J04615_at	J04615	PASS	9	51.22	PASS	13	9	26.15	1.96	1.96			
ECHS1	D13900_at	D13900	PASS	9	27.00	PASS	10	9	13.80	1.96	1.96	10q26.2-q26.3	ECHS1	small nuclear ribonucleoprotein polypeptide N
CD14	X13334_at	X13334	PASS	9	180.11	PASS	13	9	92.08	1.96	1.96			
SI64	L40392_at	L40392	PASS	8	14.00	PASS	12	8	7.17	1.95	1.95	5q22-q32	CD14 antigen	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial
														CD14 antigen
														ORF; putative

LRPAP1	M63959_at	M63959	PASS	8	28.25	PASS	13	8	14.46	1.95	1.95	1.95	LRPAP1	4p16.3	low density lipoprotein-related protein-associated protein 1 (alpha-2-macroglobulin receptor-associated protein 1)	low density lipoprotein-related protein-associated protein 1 (alpha-2-macroglobulin receptor-associated protein 1)
TXBP151	U33821_at	U33821	PASS	9	32.56	PASS	13	9	16.69	1.95	1.95	1.95	U33821		tax 1-binding protein	tax 1-binding protein
K177_ADPR	D79999_at	D79999	PASS	6	25.50	PASS	13	6	13.08	1.95	1.95	1.95	KIAA0177		similar to chicken poly(ADP-ribose) synthase, has putative hydrophobic domain in amino acid positions 638-662.	similar to chicken poly(ADP-ribose) synthase, has putative hydrophobic domain in amino acid positions 638-662.
MOZ	U47742_at	U47742	PASS	9	26.67	PASS	13	9	13.69	1.95	1.95	1.95	MOZ		hemochromatosis candidate gene V	hemochromatosis candidate gene V
HCG5	X81003_at	X81003	PASS	9	16.78	PASS	13	9	8.62	1.95	1.95	1.95	HCGV	6p21.3	small inducible cytokine A4 (homologous to mouse Mip-1b)	small inducible cytokine A4 (homologous to mouse Mip-1b)
J04130_s_at	J04130_s_at	J04130	PASS	9	27.56	PASS	13	9	14.15	1.95	1.95	1.95	SCYA4	17q21	H3 histone family, member J	H3 histone family, member J
H3F3B	M11353_at	M11353	PASS	9	245.78	PASS	13	9	126.31	1.95	1.95	1.95	H3FJ	6p22-p21.3	presenilin 1 (Alzheimer disease 3)	presenilin 1 (Alzheimer disease 3)
PSEN1	L76517_at	L76517	PASS	9	18.56	PASS	13	9	9.54	1.95	1.95	1.95	PSEN1	14q24.3	microsome glutathione S-transferase 2	microsome glutathione S-transferase 2
MGST2	U77604_at	U77604	PASS	8	19.00	PASS	13	8	9.77	1.94	1.94	1.94	MGST2	4q28-q31	myristoylated alanine-rich protein kinase C substrate (MARCKS, 80K-L)	myristoylated alanine-rich protein kinase C substrate (MARCKS, 80K-L)
MACS	D10522_at	D10522	PASS	8	13.75	PASS	13	8	7.08	1.94	1.94	1.94	MACS	6q21	proteasome (prosome, macropain) subunit, beta type, 4	proteasome (prosome, macropain) subunit, beta type, 4
PSMHSN3	D26600_at	D26600	PASS	9	46.78	PASS	13	9	24.08	1.94	1.94	1.94	PSMB4	1q21	alternatively spliced isoform in GenBank Accession Number X68148	alternatively spliced isoform in GenBank Accession Number X68148
MYL2	M21812_at	M21812	PASS	8	11.38	PASS	7	8	5.86	1.94	1.94	1.94	SHC		CDC-like kinase 2	CDC-like kinase 2
SKI	U73377_at	U73377	PASS	9	11.44	PASS	11	9	5.91	1.94	1.94	1.94	SHC		pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective tissue-activating peptide III, neutrophil-activating peptide-2)	pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective tissue-activating peptide-2)
CLK2	L29218_at	L29218	PASS	7	13.71	PASS	11	7	7.09	1.93	1.93	1.93	CLK2	1q21	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)
PPBP	M54995_at	M54995	PASS	9	251.56	PASS	13	9	130.31	1.93	1.93	1.93	PPBP	4q12-q13	ribosomal protein S27a	ribosomal protein S27a
SDHA	L21936_at	L21936	PASS	9	23.44	PASS	13	9	12.15	1.93	1.93	1.93	SDHA	5p15	G protein pathway suppressor 2	G protein pathway suppressor 2
UBA52	S79522_at	S79522	PASS	9	286.56	PASS	13	9	148.69	1.93	1.93	1.93	RPS27A	2	protease inhibitor 2 (anti-elastase), monocyte/neutrophil	protease inhibitor 2 (anti-elastase), monocyte/neutrophil
SARS	X91257_at	X91257	PASS	9	38.22	PASS	13	9	19.85	1.93	1.93	1.93	serS		putative	putative
GPS2	U28963_at	U28963	PASS	8	13.63	PASS	13	8	7.08	1.93	1.93	1.93	GPS2		oligomycin sensitivity conferral protein osep homolog. This sequence comes from Fig. 3.	oligomycin sensitivity conferral protein osep homolog. This sequence comes from Fig. 3.
ELANH2	M93056_at	M93056	PASS	8	16.13	PASS	13	8	8.38	1.92	1.92	1.92	ELANH2	6p25	Protein sequence is in conflict with the conceptual translation, insertions (-9, missing Y)	Protein sequence is in conflict with the conceptual translation, insertions (-9, missing Y)
NT5	D38524_at	D38524	PASS	8	10.00	PASS	10	8	5.20	1.92	1.92	1.92	transcript ch21		KIAA0058 gene product	KIAA0058 gene product
ATP5O	S77356_at	S77356	PASS	9	21.00	PASS	13	9	10.92	1.92	1.92	1.92	transcript ch21			
K58	D31767_at	D31767	PASS	9	108.22	PASS	13	9	56.31	1.92	1.92	1.92	KIAA0058			

YY1	M77698 at	M77698	PASS	9	13.44	PASS	9	9	7.00	1.92	1.92	YY1	14q	YY1 transcription factor	YY1 transcription factor
POLR2	U37690 at	U37690	PASS	9	51.56	PASS	13	9	26.85	1.92	1.92	hsRPH10		RNA polymerase II subunit	
CR3p211GS	L13434 at	L13434	PASS	6	12.00	PASS	8	6	6.25	1.92	1.92				
MEA	HG1869-ht	HG1869-H	PASS	9	19.33	PASS	13	9	10.08	1.92	1.92				
PSMC3	M34079_at	M34079	PASS	6	13.17	PASS	8	6	6.88	1.92	1.92	PSMC3	11p12-p13	proteasome (prosome, macropain) 26S subunit, ATPase, 3	proteasome (prosome, macropain) 26S subunit, ATPase, 3
CTGB43A	L10378 at	L10378	PASS	9	18.22	PASS	13	9	9.54	1.91	1.91				The ha2022 gene product is novel.
K84	D42043_at	D42043	PASS	9	26.00	PASS	13	9	13.62	1.91	1.91	KIAA0084			
UB ma1	U49869 ma1	U49869	PASS	9	329.78	PASS	13	9	173.00	1.91	1.91			ubiquitin	
CYBA	M21186_at	M21186	PASS	9	221.67	PASS	13	9	116.38	1.90	1.90	CYBA	16q24	cytochrome b-245 alpha polypeptide	cytochrome b-245, alpha polypeptide
PGAM1	J04173_at	J04173	PASS	9	72.56	PASS	13	9	38.15	1.90	1.90	PGAM1	10q25.3	phosphoglycerate mutase 1 (brain)	phosphoglycerate mutase 1 (brain)
MGPR ma1	X56253 ma1	X56253	PASS	9	46.33	PASS	13	9	24.38	1.90	1.90				
ITGB5	J05633 at	J05633	PASS	7	9.29	PASS	9	7	4.89	1.90	1.90	ITGB5		integrin, beta 5	integrin, beta 5
U68105 s at	U68105 s at	U68105	PASS	9	97.56	PASS	13	9	51.38	1.90	1.90				
ADAR	U10439_at	U10439	PASS	9	34.56	PASS	13	9	18.23	1.90	1.90	ADAR	1q21.1-q21.2	adenosine deaminase, RNA-specific	adenosine deaminase, RNA-specific
TP53BP2	U58334_at	U58334	PASS	6	12.00	PASS	12	6	6.33	1.89	1.89	TP53BP2	1q42.1	tumor protein p53-binding protein, 2	tumor protein p53-binding protein, 2
K135_P1M1	D50925_at	D50925	PASS	6	12.00	PASS	9	6	6.33	1.89	1.89	KIAA0135			The KIAA0135 gene is related to pim-1 oncogene.
EWSR1	X71428_at	X71428	PASS	9	72.00	PASS	13	9	38.00	1.89	1.89	FUS	16p11.2	FUS glycine rich protein	fusion, derived from t(12;16) malignant liposarcoma
PSMD7	U70735 at	U70735	PASS	9	15.44	PASS	13	9	8.15	1.89	1.89			34 kDa Mov34 homolog	similar to Mov34
ZAP112	L40399 at	L40399	PASS	6	26.50	PASS	10	6	14.00	1.89	1.89				ORE, putative
ALOX5	J03600 at	J03600	PASS	9	29.33	PASS	12	9	15.50	1.89	1.89	ALOX5	10q11.2	arachidonate 5-lipoxygenase	arachidonate 5-lipoxygenase
MEN1 ma2	U93237 ma2	U93237	PASS	6	11.67	PASS	12	6	6.17	1.89	1.89	MEN1	11q13	multiple endocrine neoplasia 1	multiple endocrine neoplasia 1
K262	D87451 at	D87451	PASS	9	54.89	PASS	13	9	29.08	1.89	1.89	KIAA0262			KIAA0262 gene product
X55448_cds1	X55448_cds1	X55448	PASS	9	27.44	PASS	13	9	14.54	1.89	1.89	G6PD		glucose-6-phosphate dehydrogenase	
E_23745	U79260_at	U79260	PASS	6	12.33	PASS	11	6	6.55	1.88	1.88				similar to human oligodendrocyte myelin glycoprotein encoded by GenBank Accession Number L05367
CBOG3955	D87119 at	D87119	PASS	8	19.75	PASS	12	8	10.50	1.88	1.88	GS955			
BLVRA	U34877 at	U34877	PASS	8	14.88	PASS	12	8	7.92	1.88	1.88	BLVRA	7p14-cen	biliverdin reductase A	biliverdin reductase A
HEXB	M23294_at	M23294	PASS	6	20.67	PASS	12	6	11.00	1.88	1.88	HEXB	5q13	hexosaminidase B (beta polypeptide)	hexosaminidase B (beta polypeptide)
AC002045_x	AC002045_x	AC002045	PASS	9	25.00	PASS	13	9	13.31	1.88	1.88	A-589H1.1		Unknown protein product	
NOL1	HG1116-HT	HG1116-H	PASS	7	12.86	PASS	13	7	6.85	1.88	1.88			form 1	
HG2090-HT	HG2090-HT	HG2090-H	PASS	9	16.89	PASS	11	9	9.00	1.88	1.88				
NDUFA4	U94586 at	U94586	PASS	9	32.44	PASS	13	9	17.31	1.87	1.87	NDUFA4		NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4 (9kD, MLRQ)	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4 (9kD, MLRQ)
K59_DMT	D31883 at	D31883	PASS	9	45.56	PASS	13	9	24.31	1.87	1.87	LIMAB1	10q25	LIM actin binding protein 1 (limatin)	LIM actin binding protein 1 (limatin)
3P25MP	L09260 at	L09260	PASS	9	16.11	PASS	13	9	8.62	1.87	1.87				

YWHAZ	M86400_at	M86400	PASS	9	116.22	PASS	13	9	62.15	1.87	1.87	YWHAZ	2p25.2-p25.1	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide
Z74792_s_at	Z74792_s_at	Z74792	PASS	5	10.80	PASS	9	5	5.78	1.87	1.87			CCAAT transcription binding factor, gamma subunit	CCAAT transcription binding factor, gamma subunit
HBG2_ma1	M91036_ma1	M91036	PASS	9	60.56	PASS	12	9	32.42	1.87	1.87	HBG1	11p15.5	hemoglobin, gamma A	hemoglobin, gamma A
COX6B_cds	AC002115_c	AC002115	PASS	9	114.11	PASS	13	9	61.23	1.86	1.86	COX6B		F25451_2	hypothetical 36.5 kDa protein most similar to ssRNA binding proteins; BLASTX similarity to (Y07952) ssRNA-binding protein [Dictyostelium discoideum] (52%) within RNP domains; and to protein C22E12.02 in chromosome I [Schizosaccharomyces pombe]
PSMHSC10	D26598_at	D26598	PASS	9	45.56	PASS	13	9	24.46	1.86	1.86	PSMB3	2q35	proteasome (prosome, macropain) subunit, beta type, 3	proteasome (prosome, macropain) subunit, beta type, 3
M14328_s_at	M14328_s_at	M14328	PASS	9	173.22	PASS	13	9	93.15	1.86	1.86	ENO1	1p36.2-p36.3	enolase 1, (alpha)	enolase 1, (alpha)
CAPN2	M23254_at	M23254	PASS	9	63.33	PASS	13	9	34.08	1.86	1.86	CAPN2	1	calpain, large polypeptide L2	calpain, large polypeptide L2
HG110-HT1	HG110-HT1	HG110-HT1	PASS	9	26.44	PASS	13	9	14.23	1.86	1.86				
U45448_s_at	U45448_s_at	U45448	PASS	8	13.63	PASS	12	8	7.33	1.86	1.86	P2RX1	17p	purinergic receptor P2X, ligand-gated ion channel, 1	purinergic receptor P2X, ligand-gated ion channel, 1
K275_SPOC	D87465_at	D87465	PASS	9	50.44	PASS	13	9	27.15	1.86	1.86	KIAA0275		KIAA0275 gene product	KIAA0275 gene product
NCL_ma1	M60858_ma1	M60858	PASS	9	73.00	PASS	13	9	39.31	1.86	1.86	NCL	2q12-qter	nucleolin	nucleolin
IRATHL60N	U09196_at	U09196	PASS	9	27.00	PASS	13	9	14.54	1.86	1.86				
CPBP	U44975_at	U44975	PASS	8	13.00	PASS	11	8	7.00	1.86	1.86	COPEB	10p15	core promoter element binding protein	core promoter element binding protein
ATP5G1	D13118_at	D13118	PASS	9	37.44	PASS	12	9	20.17	1.86	1.86	ATP5G3	2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3
EIF3	U36764_at	U36764	PASS	9	25.33	PASS	13	9	13.69	1.85	1.85	EIF3S2	1p34.1	eukaryotic translation initiation factor 3, subunit 2 (beta, 36kD)	eukaryotic translation initiation factor 3, subunit 2 (beta, 36kD)
XBP1	M31627_at	M31627	PASS	9	33.00	PASS	13	9	17.85	1.85	1.85	XBP1	22	X-box binding protein 1	X-box binding protein 1
HLA-A_f	HG3597-HT1	HG3597-HT1	PASS	9	182.11	PASS	13	9	98.62	1.85	1.85				
K77	D38521_at	D38521	PASS	9	11.67	PASS	12	9	6.33	1.84	1.84	KIAA0077			The hsa0919 gene product is novel.
KPNB1	L38951_at	L38951	PASS	7	15.86	PASS	13	7	8.62	1.84	1.84	KPNB1		karyopherin (importin) beta 1	karyopherin (importin) beta 1
NDP52	U22897_at	U22897	PASS	9	14.22	PASS	11	9	7.73	1.84	1.84	ndp52		characterized by a monoclonal antibody recognizing the encoded protein	characterized by a monoclonal antibody recognizing the encoded protein
ARF1	M84332_at	M84332	PASS	9	115.56	PASS	13	9	62.85	1.84	1.84	ARF1	1q42	ADP-ribosylation factor 1	ADP-ribosylation factor 1
DAD1	D15057_at	D15057	PASS	9	20.22	PASS	13	9	11.00	1.84	1.84	DAD1	14q11-q12	defender against cell death 1	defender against cell death 1
PPP2R5A	X52851_ma1	X52851	PASS	9	139.56	PASS	13	9	75.92	1.84	1.84			peptidylprolyl isomerase	peptidylprolyl isomerase
PPP2R5B	L42373_at	L42373	PASS	9	17.78	PASS	13	9	9.69	1.83	1.83	PPP2R5A	1q41	protein phosphatase 2A B56-alpha	protein phosphatase 2, regulatory subunit B (B56), alpha isoform
EIF4C	L18960_at	L18960	PASS	9	11.00	PASS	11	9	6.00	1.83	1.83	EIF1AY	Y chr.	eukaryotic translation initiation factor 1A, Y chromosome	eukaryotic translation initiation factor 1A, Y chromosome

GCHI	UI9523_at	UI9523	PASS	7	10.86	PASS	13	7	5.92	1.83	1.83	GCHI	14q22.1-q22.2	GTP cyclohydrolase 1 (dopa-responsive dystonia)
CD37	X14046_at	PASS	PASS	9	74.67	PASS	13	9	40.77	1.83	1.83	CD37	19p13-q13.4	GTP cyclohydrolase 1 (dopa-responsive dystonia)
K240	D87077_at	PASS	PASS	6	9.33	PASS	10	6	5.10	1.83	1.83	K1A0240		CD37 antigen
M24485_s_at	M24485_s_at	PASS	PASS	9	80.33	PASS	13	9	43.92	1.83	1.83	GSTP1	11q13	glutathione S-transferase pi
HSPD1	M22382_at	PASS	PASS	9	31.22	PASS	13	9	17.08	1.83	1.83	HSPD1		heat shock 60kD protein 1 (chaperonin)
D26156_s_at	D26156_s_at	PASS	PASS	8	13.63	PASS	13	8	7.46	1.83	1.83	SMARCA4		SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4
H1A-C f	HG658-HT6	PASS	PASS	9	320.78	PASS	13	9	175.77	1.82	1.82			
H1A-E f	HG2917-HT3	PASS	PASS	9	248.00	PASS	13	9	136.00	1.82	1.82			
K34, CLTCL	D21260_at	PASS	PASS	9	23.00	PASS	13	9	12.62	1.82	1.82	CLTCL2		clathrin, heavy polypeptide-like 2
PRKCD	D10495_at	PASS	PASS	9	30.22	PASS	12	9	16.58	1.82	1.82	35550		protein kinase C delta-type
M37238_s_a	M37238_s_a	PASS	PASS	9	11.33	PASS	9	9	6.22	1.82	1.82	PLCG2	16q24.1	phospholipase C, gamma 2 (phosphatidylinositol-specific)
RER1	AJ001421_at	PASS	PASS	9	33.89	PASS	13	9	18.62	1.82	1.82			Rer1 protein
PPR1A	HG1614-HT	PASS	PASS	9	106.56	PASS	13	9	58.62	1.82	1.82			
PPP2R4	U37352_at	PASS	PASS	7	12.57	PASS	13	7	6.92	1.82	1.82	PPP2R4	9q34	protein phosphatase 2A, regulatory subunit B' (PR 53)
HUNC18B2	AB002559_a	PASS	PASS	8	21.63	PASS	11	8	11.91	1.82	1.82			putative alternatively spliced form of gblU63533HHSU63533
J03077_s_at	J03077_s_at	PASS	PASS	9	339.89	PASS	13	9	187.54	1.81	1.81	PSAP	10q21-q22	prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy)
ARRB2	HG2059-HT7	PASS	PASS	9	24.67	PASS	13	9	13.62	1.81	1.81			
E 23652	U90911_at	PASS	PASS	9	13.00	PASS	11	9	7.18	1.81	1.81			
HG1595-HT4	HG1595-HT4	PASS	PASS	8	26.00	PASS	13	8	14.38	1.81	1.81			
CSNK1D	U29171_at	PASS	PASS	9	18.22	PASS	12	9	10.08	1.81	1.81	CSNK1D	17q25	casein kinase 1, delta
RPS3A	M84711_at	PASS	PASS	9	298.78	PASS	13	9	165.62	1.80	1.80	RPS3A	4q31.2-q31.3	ribosomal protein S3A
GLUL	X59834_at	PASS	PASS	9	23.00	PASS	12	9	12.75	1.80	1.80	GLUL	1q31	glutamate-aminomycin ligase (glutamine synthase)
IL4R	X52425_at	PASS	PASS	9	26.22	PASS	11	9	14.55	1.80	1.80	IL4R	16p11.2-p12.1	interleukin 4 receptor
CSTB ma1	U46692_ma1	PASS	PASS	9	47.22	PASS	13	9	26.23	1.80	1.80	CSTB	21q22.3	cystatin B (stefin B)
M22348_s_at	M22348_s_at	PASS	PASS	8	11.38	PASS	9	8	6.33	1.80	1.80	UQBIP		ubiquitinone-binding protein precursor
RPS17	M18000_at	PASS	PASS	9	464.56	PASS	13	9	258.69	1.80	1.80	RPS17	11pter-p13 or 15q	ribosomal protein S17
RPLP0	M17885_at	PASS	PASS	9	436.11	PASS	13	9	243.00	1.79	1.79	RPLP0	12	ribosomal protein, large, P0
YRS28	D14530_at	PASS	PASS	9	367.89	PASS	13	9	205.31	1.79	1.79	RPS23	5q	ribosomal protein S23
CBFB	L20298_at	PASS	PASS	9	21.78	PASS	13	9	12.15	1.79	1.79	CBFB	16q22.1	core-binding factor, beta subunit
CANX	L10284_at	PASS	PASS	9	41.89	PASS	13	9	23.38	1.79	1.79	CANX	5q35	calnexin
HLARX	U89505_at	PASS	PASS	8	17.75	PASS	13	8	9.92	1.79	1.79	RBM4	11q13	RNA binding motif protein 4
ZFP	U69645_at	PASS	PASS	8	10.13	PASS	12	8	5.67	1.79	1.79			C2H2 type zinc finger
SU11	L26247_at	PASS	PASS	9	177.22	PASS	13	9	99.38	1.78	1.78	su1101		isolol of yeast su11 and rice gos2, putative
VDAC1	L06132_at	PASS	PASS	8	15.50	PASS	13	8	8.69	1.78	1.78	VDAC1	5q31	voltage-dependent anion channel 1
L12711_s_at	L12711_s_at	PASS	PASS	9	67.89	PASS	13	9	38.08	1.78	1.78	TKT	3p14.3	transketolase (Wernicke-Korsakoff syndrome)





SELL	M25280_at	M25280	PASS	9	130.11	PASS	13	9	74.38	1.75	1.75	LNHR			lymph node homing receptor precursor
M26311_s_at	M26311_s_at	M26311	PASS	9	301.44	PASS	13	9	172.38	1.75	1.75	S100A9	1q12-q22	S100 calcium-binding protein A9 (calgranulin B)	S100 calcium-binding protein A9 (calgranulin B)
ANX2	D00017_at	D00017	PASS	9	88.33	PASS	13	9	50.62	1.75	1.75	ANX2	15q21-q22	annexin II (lipocortin II; calpactin I, heavy polypeptide)	annexin II (lipocortin II; calpactin I, heavy polypeptide)
K257_COSC	D87446_at	D87446	PASS	9	9.89	PASS	12	9	5.67	1.75	1.75	KIAA0257			Similar to a C.elegans protein encoded in cosmid C27F2 (U40419)
K239_K215	D87076_at	D87076	PASS	7	19.00	PASS	10	7	10.90	1.74	1.74	KIAA0239			similar to human bromodomain protein BR140(UC2069)
S7871_s_at	S7871_s_at	S7871	PASS	6	12.00	PASS	10	6	6.90	1.74	1.74				
X89109_s_at	X89109_s_at	X89109	PASS	9	107.22	PASS	13	9	61.69	1.74	1.74			coronin homologue	
S82447_s_at	S82447_s_at	S82447	PASS	8	10.25	PASS	10	8	5.90	1.74	1.74	GCN5L1	12q13-q14	GCN5 (general control of amino-acid synthesis, yeast, homolog)-like 1	GCN5 (general control of amino-acid synthesis, yeast, homolog)-like 1
FCN1	D83920_at	D83920	PASS	9	244.89	PASS	13	9	141.00	1.74	1.74	FCN1	9q34	ficollin (collagen/fibrinogen domain-containing) 1	ficollin (collagen/fibrinogen domain-containing) 1
HLA-DMB	U15085_at	U15085	PASS	9	54.22	PASS	13	9	31.23	1.74	1.74	HLA-DMB	6p21.3	major histocompatibility complex, class II, DM beta	major histocompatibility complex, class II, DM beta
CCND2	D13639_at	D13639	PASS	9	39.11	PASS	13	9	22.54	1.74	1.74	CCND2	12p13	cyclin D2	cyclin D2
CSNK1G2	U89896_at	U89896	PASS	6	9.83	PASS	9	6	5.67	1.74	1.74			casein kinase I gamma 2	
TAF2H	U13991_at	U13991	PASS	9	33.44	PASS	13	9	19.31	1.73	1.73	taf1130		TATA-binding protein associated factor 30 kDa subunit	
M55409_s_at	M55409_s_at	M55409	PASS	9	258.78	PASS	13	9	149.46	1.73	1.73	EEF1G		eukaryotic translation elongation factor 1 gamma	eukaryotic translation elongation factor 1 gamma
W52B2_f	HG688-HT68	HG688-HT68	PASS	8	61.25	PASS	13	8	35.38	1.73	1.73				
TRNASTL	U07424_at	U07424	PASS	7	14.00	PASS	11	7	8.09	1.73	1.73	FARSL		phenylalanine-tRNA synthetase like	phenylalanine-tRNA synthetase-like
EIF2B	M29536_at	M29536	PASS	9	24.89	PASS	13	9	14.38	1.73	1.73	EIF2B2		eukaryotic translation initiation factor 2, subunit 2 (beta, 38kD)	eukaryotic translation initiation factor 2, subunit 2 (beta, 38kD)
E_23722	U90909_at	U90909	PASS	8	9.75	PASS	11	8	5.64	1.73	1.73				
LGALS3	M57710_at	M57710	PASS	9	66.89	PASS	13	9	38.69	1.73	1.73	LGALS3	1p13	lectin, galactoside-binding, soluble, 3 (galactin 3)	lectin, galactoside-binding, soluble, 3 (galactin 3)
PKUA	AB004884_a	AB004884	PASS	7	12.29	PASS	8	7	7.13	1.72	1.72			PKU-alpha	
J05016_ma1	J05016_ma1	J05016	PASS	8	9.88	PASS	11	8	5.73	1.72	1.72	ERP70	7; 10	protein disulfide isomerase related protein (calcium-binding protein, intestinal-related)	protein disulfide isomerase related protein (calcium-binding protein, intestinal-related)
Y09392_s_at	Y09392_s_at	Y09392	PASS	9	11.67	PASS	13	9	6.77	1.72	1.72	wsl-1		WSL-S2 protein	truncated form of T-lymphocyte-specific protein tyrosine kinase p56lck, this aberrant message encoding primarily the SH2 and SH3 domains of p56lck was observed by northern hybridization and PCR amplification in poly-A selected RNA from two human leukemic T-cell lines.
U23852_s_at	U23852_s_at	U23852	PASS	9	66.89	PASS	13	9	38.85	1.72	1.72	lck		p56lck	

P4HB	J02783_at	J02783	PASS	5	30.20	PASS	11	5	17.55	1.72	1.72	P4HB	17q25	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55)	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55)	
DYRK	D86550_at	D86550	PASS	9	18.67	PASS	13	9	10.85	1.72	1.72	hMNB		human homolog of Drosophila mmb (minibrain) gene	human homolog of Drosophila mmb (minibrain) gene	
PSMCI	L02426_at	L02426	PASS	9	25.67	PASS	13	9	14.92	1.72	1.72	PSMCI	19p13.3	proteasome (prosome, macropain) 26S subunit, ATPase, 1	proteasome (prosome, macropain) 26S subunit, ATPase, 1	
CD1D	L38820_at	L38820	PASS	8	12.50	PASS	11	8	7.27	1.72	1.72	CD1D		CD1D antigen	CD1D antigen	
RPL9	U09953_at	U09953	PASS	9	318.56	PASS	13	9	185.46	1.72	1.72	RPL9	4p13	ribosomal protein L9	ribosomal protein L9	
U59877_s_at	U59877_s_at	U59877	PASS	6	15.67	PASS	8	6	9.13	1.72	1.72	RAB31		low-Mr GTP-binding protein of the Rab subfamily	low-Mr GTP-binding protein of the Rab subfamily	
GALT	M60091_at	M60091	PASS	9	11.44	PASS	9	9	6.67	1.72	1.72	GALT		galactose-1-phosphate uridylyl transferase	galactose-1-phosphate uridylyl transferase	
MARS	X94754_at	X94754	PASS	9	13.33	PASS	13	9	7.77	1.72	1.72	MARS	12	yeast methionyl-tRNA synthetase homolog	methionine-tRNA synthetase	
SI53	L40391_at	L40391	PASS	9	26.44	PASS	12	9	15.42	1.72	1.72					
CCNI	D50310_at	D50310	PASS	9	99.33	PASS	13	9	57.92	1.71	1.71					
K99_PUML	D43951_at	D43951	PASS	9	12.00	PASS	11	9	7.00	1.71	1.71	KIAA0099		KIAA0099 gene product	KIAA0099 gene product	
SRI	M81637_at	M81637	PASS	8	9.00	PASS	8	8	5.25	1.71	1.71	grancalcin		putative	putative	
NDUFS8	U65579_at	U65579	PASS	6	9.00	PASS	8	6	5.25	1.71	1.71	NDUFS8	11q13	NADH dehydrogenase (ubiquinone) Fe-S protein 8 (23kD) (NADH-coenzyme Q reductase)	NADH dehydrogenase (ubiquinone) Fe-S protein 8 (23kD) (NADH-coenzyme Q reductase)	
E_23693	U79254_at	U79254	PASS	9	20.56	PASS	13	9	12.00	1.71	1.71					
K272_HYPC	D87462_at	D87462	PASS	6	11.50	PASS	7	6	6.71	1.71	1.71	BAP1	3p21.31-p21.2	BRCA1 associated protein-1 (ubiquitin carboxy-terminal hydrolase)	BRCA1 associated protein-1 (ubiquitin carboxy-terminal hydrolase)	
A4	L09604_at	L09604	PASS	9	80.22	PASS	13	9	46.85	1.71	1.71	PLP2	Xp11.23	proteolipid protein 2 (colonic epithelium-enriched)	proteolipid protein 2 (colonic epithelium-enriched)	
SLC6A8_ma	U36341_ma	U36341	PASS	9	13.11	PASS	9	9	7.67	1.71	1.71	SLC6A8		creatine transporter	creatine transporter	
TFAP3D	U91930_at	U91930	PASS	9	20.11	PASS	13	9	11.77	1.71	1.71	ADTD	19p13.3	adaptin, delta	adaptin, delta	
SEPW1	U67171_at	U67171	PASS	9	25.89	PASS	13	9	15.15	1.71	1.71	SEPW1		selenoprotein W, 1	selenoprotein W, 1	
P542	L38696_at	L38696	PASS	6	17.33	PASS	13	6	10.15	1.71	1.71			huhRy; hnRNP C3, N-terminus autoantigen p542	huhRy; hnRNP C3, N-terminus autoantigen p542	
ERCC5	X69978_at	X69978	PASS	8	12.88	PASS	9	8	7.56	1.70	1.70	ERCC5	13q22-q34	XPG complementing protein	excision repair cross-complementing rodent repair deficiency, complementation group 5 (xeroderma pigmentosum, complementation group G (Cockayne syndrome))	
ARF4	M36341_at	M36341	PASS	9	17.56	PASS	13	9	10.31	1.70	1.70	ARF4		ADP-ribosylation factor 4	ADP-ribosylation factor 4	
POLRMP	U75370_at	U75370	PASS	7	10.43	PASS	8	7	6.13	1.70	1.70	POLRMT	19p13.3	mitochondrial RNA polymerase	polymyrase (RNA) mitochondrial (DNA directed)	
LUMAN	AF009368_at	AF009368	PASS	7	17.29	PASS	11	7	10.18	1.70	1.70			Luman		basic leucine zipper (BZIP) protein; binds to herpes simplex virus VP16 associated host cellular factor (HCF); member of CREB/ATF protein family, mouse LZIP homolog

SAP61	U08815_at	U08815	PASS	8	10.75	PASS	9	8	6.33	1.70	1.70	SAP 61	similar to yeast PRP9, Swiss-Prot Accession Number P19736
ITK	L10717_at	L10717	PASS	9	15.67	PASS	13	9	9.23	1.70	1.70	tyrosine kinase	2024-2555 unique domain; 2556-2708 SH3 domain; 2750-3044 SH2 domain (binds phosphotyrosine-containing proteins); 3095-3884 kinase domain (phosphorylation of tyrosine residues) ; putative
APFX-HUM6	APFX-HUM6	APFX-HUN	PASS	7	14.14	PASS	9	7	8.33	1.70	1.70		
EIF23	U94855_at	U94855	PASS	9	60.00	PASS	13	9	35.38	1.70	1.70	EIF3S5	eukaryotic translation initiation factor 3, subunit 5 (epsilon, 47kD)
U50079_s_at	U50079_s_at	U50079	PASS	7	22.43	PASS	13	7	13.23	1.70	1.70		histone deacetylase HD1
ISG20	U88964_at	U88964	PASS	9	49.00	PASS	13	9	28.92	1.69	1.69	ISG20	interferon stimulated gene (20kD)
CD81	M33680_at	M33680	PASS	9	76.22	PASS	13	9	45.00	1.69	1.69	CD81	CD81 antigen (target of antiproliferative antibody 1)
U19713_s_at	U19713_s_at	U19713	PASS	9	45.33	PASS	13	9	26.77	1.69	1.69	IRT-1	interferon gamma responsive transcript
APRT_ma1	Y00486_ma1	Y00486	PASS	9	43.22	PASS	13	9	25.54	1.69	1.69	APRT	adenine phosphoribosyltransferase
NF45	U10323_at	U10323	PASS	9	24.33	PASS	13	9	14.38	1.69	1.69	ILF2	interleukin enhancer binding factor 2, 45kD
IP30	J03909_at	J03909	PASS	9	159.78	PASS	13	9	94.54	1.69	1.69		gamma-interferon-inducible protein precursor
ORF	M68864_at	M68864	PASS	9	36.78	PASS	13	9	21.77	1.69	1.69		ORF
RPL27A	U14968_at	U14968	PASS	9	369.33	PASS	13	9	218.85	1.69	1.69	RPL27A	ribosomal protein L27a
RENT1	D86988_at	D86988	PASS	9	27.11	PASS	13	9	16.08	1.69	1.69	RENT1	regulator of nonsense transcripts 1
MOV34L	D50063_at	D50063	PASS	9	19.11	PASS	12	9	11.33	1.69	1.69	PSMD7	16q23-q24 proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mov34 homolog)
FHL1	U60115_at	U60115	PASS	9	10.89	PASS	13	9	6.46	1.69	1.69	FHL1	Xq27.2
COX5B	M19961_at	M19961	PASS	8	35.88	PASS	13	8	21.31	1.68	1.68	COX5B	2cen-q13 cytochrome c oxidase subunit Vb
EIF4G2	U73824_at	U73824	PASS	9	48.56	PASS	13	9	28.85	1.68	1.68	EIF4G2	11p15
K70_KARS	D31890_at	D31890	PASS	9	31.44	PASS	13	9	18.69	1.68	1.68	KIAA0070	eukaryotic translation initiation factor 4 gamma, 2
CDC37L	U43077_at	U43077	PASS	9	24.44	PASS	13	9	14.54	1.68	1.68		CDC37 homolog
SSBP	M94556_at	M94556	PASS	9	23.78	PASS	13	9	14.15	1.68	1.68	SSBP	single-stranded DNA-binding protein
RG33	U27655_at	U27655	PASS	8	8.25	PASS	12	8	4.92	1.68	1.68		RGp3
K190_UBP3	D80012_at	D80012	PASS	8	14.25	PASS	12	8	8.50	1.68	1.68	USP10	ubiquitin specific protease 10
FLJ1_ma1	U80184_ma1	U80184	PASS	7	18.43	PASS	13	7	11.00	1.68	1.68	FLJ1	flightless 1 (Drosophila) homolog
AIM1	U83115_at	U83115	PASS	9	20.44	PASS	13	9	12.23	1.67	1.67	AIM1	non-lens beta gamma-crystallin like protein
TATSF1	U76992_at	U76992	PASS	7	10.29	PASS	13	7	6.15	1.67	1.67	Tat-SF1	similar to EWS and FUS/TLS77

K235_K99	D87078_at	D87078	PASS	5	23.40	PASS	13	5	14.00	1.67	1.67	KIAA0235			similar to D melanogaster pumilio protein (S22020); similar to human KIAA0099 protein(D43951)
HSPB1	U12404_at	U12404	PASS	9	340.44	PASS	13	9	203.69	1.67	1.67		Csa-19		
K205_COSC	D86960_at	D86960	PASS	9	9.89	PASS	12	9	5.92	1.67	1.67	KIAA0205			KIAA0205 gene product
CTBP1	U37408_at	U37408	PASS	9	19.67	PASS	13	9	11.77	1.67	1.67	CTBP1	4p16		C-terminal binding protein 1
EBVSRAP	HG662-HT6	HG662-HT	PASS	9	150.89	PASS	13	9	90.38	1.67	1.67				
ARHGDIB	L20688_at	L20688	PASS	9	315.00	PASS	13	9	188.69	1.67	1.67	ARHGDIB	12p12.3		Rho GDP dissociation inhibitor (GDI) beta
LTA4H	J03459_at	J03459	PASS	9	78.78	PASS	13	9	47.23	1.67	1.67	LTA4H	12q22		leukotriene A4 hydrolase
ELP1	M88458_at	M88458	PASS	9	12.44	PASS	13	9	7.46	1.67	1.67				
NP220	D83032_at	D83032	PASS	9	10.00	PASS	13	9	6.00	1.67	1.67				unsure initial methionine; putative
TAP	U80073_at	U80073	PASS	9	14.44	PASS	12	9	8.67	1.67	1.67	TAP			tip associating protein
EV12B	M60830_at	M60830	PASS	8	20.25	PASS	13	8	12.15	1.67	1.67				open reading frame
K249_K188	D87436_at	D87436	PASS	8	8.88	PASS	12	8	5.33	1.66	1.66	KIAA0249			KIAA0249 gene product
CIT987SK	U95740_mal	U95740	PASS	9	14.00	PASS	12	9	8.42	1.66	1.66	A-362G6.1			Unknown gene product
NASP	M97856_at	M97856	PASS	8	12.88	PASS	8	8	7.75	1.66	1.66	NASP			nuclear autoantigenic sperm protein (histone-binding)
K94_MEAP1	D42084_at	D42084	PASS	8	11.63	PASS	13	8	7.00	1.66	1.66	KIAA0094			KIAA0094 gene product is related to S cerevisiae methionine aminopeptidase.
L10333_s_at	L10333_s_at	L10333	PASS	5	9.80	PASS	11	5	5.91	1.66	1.66	NSP			neuroendocrine-specific protein A
H2A1L	U90551_at	U90551	PASS	9	42.22	PASS	13	9	25.46	1.66	1.66	H2A1L			histone 2A-like protein
K49_IAB3B	D30756_at	D30756	PASS	9	10.44	PASS	13	9	6.31	1.66	1.66	KIAA0049			KIAA0049 gene product
DNAPK	U85611_at	U85611	PASS	9	35.89	PASS	13	9	21.69	1.65	1.65	KIP			DNA-PK interaction protein
D13720_s_at	D13720_s_at	D13720	PASS	8	14.25	PASS	13	8	8.62	1.65	1.65				ITK
K241_COST	D63877_at	D63877	PASS	6	8.50	PASS	7	6	5.14	1.65	1.65	KIAA0157			originally named lyk KIAA0157 gene product is novel.
RCH1	U28386_at	U28386	PASS	7	8.86	PASS	11	7	5.36	1.65	1.65	KPNA2	17q23.1-q23.3		karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
K37_ADCY	D25538_at	D25538	PASS	9	17.78	PASS	13	9	10.77	1.65	1.65	ADCY7	16q12-q13		adenylate cyclase 7
RS1	M24194_at	M24194	PASS	9	326.89	PASS	13	9	198.15	1.65	1.65	H12-3			homologue, putative
IEFSSP9502	L07758_at	L07758	PASS	9	9.44	PASS	11	9	5.73	1.65	1.65				nuclear phosphoprotein (similarity to Saccharomyces cerevisiae PWP1 protein)
K53_CDC42	D29642_at	D29642	PASS	9	27.89	PASS	12	9	16.92	1.65	1.65	KIAA0053			KIAA0053 gene product
ABR	U01147_at	U01147	PASS	9	9.89	PASS	12	9	6.00	1.65	1.65	ABR	17p13.3		active BCR-related gene
SET	M93651_at	M93651	PASS	9	24.33	PASS	13	9	14.77	1.65	1.65	SET	9q34		SET translocation (myeloid leukemia-associated)
K38	D26068_at	D26068	PASS	9	54.22	PASS	13	9	32.92	1.65	1.65	WBSCR1	7q11.23		Williams-Beuren syndrome chromosome region 1
PTPCAAX1	U48296_at	U48296	PASS	7	8.43	PASS	8	7	5.13	1.64	1.64	PTPA1	6q12		protein tyrosine phosphatase type IVA, member 1
U01691_s_at	U01691_s_at	U01691	PASS	9	17.44	PASS	13	9	10.62	1.64	1.64	ANX5	4q28-q32		anexin V (endonexin II)
M16591_s_at	M16591_s_at	M16591	PASS	9	29.44	PASS	13	9	17.92	1.64	1.64	HCK	20q11-q12		hemopoietic cell kinase
K102_SPC25	D14658_at	D14658	PASS	9	22.11	PASS	13	9	13.46	1.64	1.64	KIAA0102			KIAA0102 gene product
E_23815	U90916_at	U90916	PASS	8	11.88	PASS	13	8	7.23	1.64	1.64				

NFE2L2	S74017_at	S74017	PASS	5	11.00	PASS	10	5	6.70	1.64	1.64	Nrf2	Nrf2	NFE2-like basic leucine zipper transcriptional activator; This sequence comes from Fig. 1
MTH1	D16581_at	D16581	PASS	8	17.00	PASS	11	8	10.36	1.64	1.64	MTH1	7p22	mutT (E. coli) human homolog (8-oxo-7,8-dihydroguanosine triphosphatase)
FKHR	U36922_at	U36922	PASS	9	17.78	PASS	13	9	10.85	1.64	1.64	KIAA0105	6	gene predicted from cDNA with a complete coding sequence
KI05	D14661_at	D14661	PASS	7	8.57	PASS	13	7	5.23	1.64	1.64	CAST	5q14-q22	calpastatin
CAST	D16217_at	D16217	PASS	9	20.67	PASS	13	9	12.62	1.64	1.64	DOCK2		dedicator of cyto-kinesis 2
K209	DOCK2	D86964	PASS	9	20.78	PASS	13	9	12.69	1.64	1.64	rtvp-1		
X91911_s at	X91911_s at	X91911	PASS	8	21.13	PASS	13	8	12.92	1.63	1.63	TCF7		
DAPM	APFX-DapX	APFX-Dap	PASS	9	505.56	PASS	13	9	309.31	1.63	1.63			
TCF7	X59871_at	X59871	PASS	9	45.22	PASS	13	9	27.69	1.63	1.63		5q31	transcription factor 7 (T-cell specific, HMG-box)
RPS13	HG821-HT821	HG821-HT	PASS	9	277.00	PASS	13	9	169.77	1.63	1.63	ARD1		N-acetyltransferase, homolog of S cerevisiae ARD1
X77588_s at	X77588_s at	X77588	PASS	8	10.88	PASS	12	8	6.67	1.63	1.63		Xq28	beta-tubulin
V00599_s at	V00599_s at	V00599	PASS	9	49.78	PASS	13	9	30.54	1.63	1.63	TP53	17p13.1	tumor protein p53 (Li-Fraumeni syndrome)
TP53	M22898_at	M22898	PASS	7	8.00	PASS	11	7	4.91	1.63	1.63	CREBL1	6p21.3	cAMP responsive element binding protein-like 1
U31903_s at	U31903_s at	U31903	PASS	7	16.14	PASS	11	7	9.91	1.63	1.63			heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)
SLC1A7	U53347_at	U53347	PASS	7	13.57	PASS	12	7	8.33	1.63	1.63	HNRPU		transforming growth factor, beta-induced, 68kD
D13413_ma	D13413_ma	D13413	PASS	9	438.11	PASS	13	9	269.08	1.63	1.63	TGFBI	5q31	The KIAA0122 gene product is novel.
TGFBI	M77349_at	M77349	PASS	9	42.67	PASS	13	9	26.23	1.63	1.63	KIAA0122		amino-terminal enhancer of split nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha
K122	D50912_at	D50912	PASS	6	8.33	PASS	8	6	5.13	1.63	1.63	AES	19p13.3	KIAA0026 gene product
AES	U04241_at	U04241	PASS	9	65.33	PASS	13	9	40.23	1.62	1.62	NFKBIA	14q13	
MAD3	M69043_at	M69043	PASS	9	41.33	PASS	13	9	25.46	1.62	1.62			
NME2	HG1153-HT	HG1153-H	PASS	9	42.00	PASS	13	9	25.92	1.62	1.62	CD3G		Ti antigen CD3-associated protein precursor
K26	D14812_at	D14812	PASS	9	36.44	PASS	12	9	22.50	1.62	1.62	MANB	19cen-q13.1	mannosidase, alpha B, lysosomal
HG4312-HT	HG4312-HT	HG4312-H	PASS	9	48.33	PASS	13	9	29.85	1.62	1.62	CD36	7q11.2	CD36 antigen (collagen type I receptor, thrombospondin receptor)
TCRG	M30894_at	M30894	PASS	9	19.56	PASS	13	9	12.08	1.62	1.62			
U05572_s at	U05572_s at	U05572	PASS	9	27.89	PASS	13	9	17.23	1.62	1.62	BLVRB	19q13.1-q13.2	biliverdin reductase B (flavin reductase (NADPH))
M98399_s at	M98399_s at	M98399	PASS	8	15.38	PASS	12	8	9.50	1.62	1.62	KIAA0147		The KIAA0147 gene product is related to adenylyl cyclase.
BLVRB	D26308_at	D26308	PASS	9	36.00	PASS	12	9	22.25	1.62	1.62	KIAA0115		oligosaccharyltransferase 48 kDa subunit (M98392).
K147_ADCY	D63481_at	D63481	PASS	7	9.57	PASS	12	7	5.92	1.62	1.62			
K115_OLIG	D29643_at	D29643	PASS	9	26.22	PASS	13	9	16.23	1.62	1.62	RPL11	1	ribosomal protein L11
RPL11	X79234_at	X79234	PASS	9	299.56	PASS	13	9	185.62	1.61	1.61			

HNRPA2B1	M29064_at	M29064	PASS	9	34.00	PASS	13	9	21.08	1.61	1.61	1.61	HNRPA2B1	7p15	heterogeneous nuclear ribonucleoprotein A2/B1	heterogeneous nuclear ribonucleoprotein A2/B1
PSM27	AB003177_at	AB003177	PASS	7	16.71	PASS	11	7	10.36	1.61	1.61	1.61	PSMD9	12q24.31-q24.32	proteasome (prosome, macropain) 26S subunit, non-ATPase, 9	proteasome (prosome, macropain) 26S subunit, non-ATPase, 9
D42040_s_at	D42040_s_at	D42040	PASS	8	20.38	PASS	11	8	12.64	1.61	1.61	1.61	KIAA9001	11q13.3	aryl hydrocarbon receptor-interacting protein	KIAA9001 gene product
ARA9	U78521_at	U78521	PASS	9	54.56	PASS	13	9	33.85	1.61	1.61	1.61	AIP		aryl hydrocarbon receptor-interacting protein	aryl hydrocarbon receptor-interacting protein
K245_PRA4	D87432_at	D87432	PASS	8	7.88	PASS	9	8	4.89	1.61	1.61	1.61	SLC7A6		solute carrier family 7 (cationic amino acid transporter, y+ system), member 6	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6
GMFB	AB001106_at	AB001106	PASS	7	10.14	PASS	13	7	6.31	1.61	1.61	1.61	GMFB		glia maturation factor, beta	glia maturation factor, beta
K136	D50926_at	D50926	PASS	8	11.50	PASS	13	8	7.15	1.61	1.61	1.61	KIAA0136		The KIAA0136 gene product is novel.	The KIAA0136 gene product is novel.
BM11	L13689_at	L13689	PASS	9	9.89	PASS	13	9	6.15	1.61	1.61	1.61	BM11	10p13	murine leukemia viral (bmi-1) oncogene homolog	murine leukemia viral (bmi-1) oncogene homolog
MVK	L77213_at	L77213	PASS	6	8.83	PASS	10	6	5.50	1.61	1.61	1.61			pinin, desmosome associated protein	pinin, desmosome associated protein
PNN	U77718_at	U77718	PASS	8	10.50	PASS	13	8	6.54	1.61	1.61	1.61	PNN		13kD differentiation-associated protein	13kD differentiation-associated protein
13KDDAP	U34343_at	U34343	PASS	9	27.67	PASS	13	9	17.23	1.61	1.61	1.61			putative DNA dependent ATPase and helicase	putative DNA dependent ATPase and helicase
AF000424_s	AF000424_s	AF000424	PASS	8	68.25	PASS	13	8	42.54	1.60	1.60	1.60	LST1		transducin beta-2 subunit	transducin beta-2 subunit
U72936_s_at	U72936_s_at	U72936	PASS	8	9.38	PASS	13	8	5.85	1.60	1.60	1.60	ATRX		eukaryotic translation elongation factor 1 beta 2	eukaryotic translation elongation factor 1 beta 2
M36429_s_at	M36429_s_at	M36429	PASS	7	15.29	PASS	13	7	9.54	1.60	1.60	1.60	EEF1B2	2	capping protein alpha subunit isoform 1	capping protein alpha subunit isoform 1
EEF1B1	X60489_at	X60489	PASS	9	134.56	PASS	13	9	84.00	1.60	1.60	1.60			ribosomal protein L28	ribosomal protein L28
CAPZA	U56637_at	U56637	PASS	9	62.33	PASS	13	9	38.92	1.60	1.60	1.60			dishevelled 3 (homologous to Drosophila dsh)	dishevelled 3 (homologous to Drosophila dsh)
RPL28	U14969_at	U14969	PASS	9	444.22	PASS	13	9	277.62	1.60	1.60	1.60	RPL28	19q13.4	collagen, type XI, alpha 1	collagen, type XI, alpha 1
K208_DISH3	D86963_at	D86963	PASS	6	9.33	PASS	12	6	5.83	1.60	1.60	1.60	DVL3	3q27	KIAA0063 gene product	KIAA0063 gene product
COL11A1	J04177_at	J04177	PASS	6	7.00	PASS	8	6	4.38	1.60	1.60	1.60	COL11A1	1p21	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2
PD123	D14878_at	D14878	PASS	8	10.13	PASS	12	8	6.33	1.60	1.60	1.60	D123		chitinase 3-like 2	chitinase 3-like 2
K63	D31884_at	D31884	PASS	9	11.33	PASS	11	9	7.09	1.60	1.60	1.60	KIAA0063		cell division cycle 10 (homologous to CDC10 of S. cerevisiae)	cell division cycle 10 (homologous to CDC10 of S. cerevisiae)
ATP5G2_ma	X69908_ma	X69908	PASS	9	48.67	PASS	13	9	30.46	1.60	1.60	1.60	ATP5G2	12		
PAP	X76770_at	X76770	PASS	7	10.14	PASS	11	7	6.36	1.59	1.59	1.59				
U49835_s_at	U49835_s_at	U49835	PASS	9	13.67	PASS	12	9	8.58	1.59	1.59	1.59	CHI3L2	1p13.3		
CDC10	S72008_at	S72008	PASS	9	32.33	PASS	13	9	20.31	1.59	1.59	1.59	CDC10			

IQGAP1	L33075_at	L33075	PASS	9	42.00	PASS	13	9	26.38	1.59	1.59	IQGAP1	ras GTPase-activating-like protein	amino acid feature: IQ calmodulin-binding domains, aa 740 .. 865; amino acid feature: N-terminal repeats, aa 210 .. 680; amino acid feature: Sar1 homologous region, aa 920 .. 1657; amino acid feature: putative GAP catalytic domain, aa 1000 .. 1270
IMPDH2_ma	L33842_ma	L33842	PASS	9	15.89	PASS	13	9	10.00	1.59	1.59	IMPDH2	IMP (inosine monophosphate) dehydrogenase 2	IMP (inosine monophosphate) dehydrogenase 2
RAND	D25274_at	D25274	PASS	9	26.33	PASS	13	9	16.62	1.58	1.58			
GPSI	U20285_at	U20285	PASS	9	15.11	PASS	13	9	9.54	1.58	1.58	GPSI	G protein pathway suppressor 1	G protein pathway suppressor 1
LYZ_f	J03801_f_at	J03801	PASS	9	176.33	PASS	13	9	111.31	1.58	1.58	LYZ	lysosome	lysosome (renal amyloidosis)
SRD5A1	M32313_at	M32313	PASS	7	8.14	PASS	7	7	5.14	1.58	1.58	SRD5A1	steroid-5-alpha-reductase, alpha polypeptide 1	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5-alpha-steroid delta 4-dehydrogenase alpha 1)
RPS24L	M81757_at	M81757	PASS	9	420.33	PASS	13	9	265.54	1.58	1.58	RPS19	ribosomal protein S19	ribosomal protein S19
ARC20	AF006087_at	AF006087	PASS	8	19.63	PASS	10	8	12.40	1.58	1.58	ARC20	20 kD subunit of the Arp2/3 protein complex	20 kD subunit of the Arp2/3 protein complex
ARHA	L25080_at	L25080	PASS	9	143.56	PASS	13	9	90.77	1.58	1.58	ARHA	GTP-binding protein	ras homolog gene family, member A
RPLP1	M17886_at	M17886	PASS	9	381.67	PASS	13	9	241.38	1.58	1.58	RPLP1	ribosomal protein, large, P1	ribosomal protein, large, P1
PRKAR2B	M31158_at	M31158	PASS	8	17.75	PASS	13	8	11.23	1.58	1.58	PRKAR2B	protein kinase, cAMP-dependent, regulatory, type II, beta	protein kinase, cAMP-dependent, regulatory, type II, beta
BAG1	Z35491_at	Z35491	PASS	8	9.63	PASS	11	8	6.09	1.58	1.58	BAG1	BCL2-associated athanogene	BCL2-associated athanogene
RPS20	HG1800-HT	HG1800-H	PASS	9	384.89	PASS	13	9	243.62	1.58	1.58			
L43575_s_at	L43575_s_at	L43575	PASS	8	10.63	PASS	11	8	6.73	1.58	1.58			
CHSI	U67615_at	U67615	PASS	7	10.00	PASS	12	7	6.33	1.58	1.58	CHSI	Chediak-Higashi syndrome 1	Chediak-Higashi syndrome 1
RAP1A	M22995_at	M22995	PASS	8	16.13	PASS	13	8	10.23	1.58	1.58	RAP1A	RAP1A, member of RAS oncogene family	RAP1A, member of RAS oncogene family
L04483_s_at	L04483_s_at	L04483	PASS	9	437.33	PASS	13	9	277.77	1.57	1.57	RPS21	ribosomal protein S21	ribosomal protein S21
KSRP	U94832_at	U94832	PASS	9	8.44	PASS	11	9	5.36	1.57	1.57	KSRP	RNA binding protein, KH type RNA binding domain; alternative splicing regulator; cooperative complex formation	RNA binding protein, KH type RNA binding domain; alternative splicing regulator; cooperative complex formation
PSMB6	D29012_at	D29012	PASS	9	24.44	PASS	13	9	15.54	1.57	1.57	PSMB6	proteasome subunit Y	proteasome (prosome, macropain) subunit, beta type, 6
RLIP76	L42542_at	L42542	PASS	8	11.25	PASS	13	8	7.15	1.57	1.57	RLIP76	RLIP76 protein	
LMO2_ma1	X61118_ma1	X61118	PASS	8	15.00	PASS	13	8	9.54	1.57	1.57	TTG-2a/RBTN-2a		
BPGM	X04327_at	X04327	PASS	7	7.86	PASS	11	7	5.00	1.57	1.57	BPGM	2,3-bisphosphoglycerate mutase	2,3-bisphosphoglycerate mutase
MTHFD	J04031_at	J04031	PASS	7	7.86	PASS	8	7	5.00	1.57	1.57	MTHFD	5,10-methylenetetrahydrofolate dehydrogenase, 5,10-methylenetetrahydrofolate cyclohydrolase, 10-formyltetrahydrofolate synthetase	5,10-methylenetetrahydrofolate dehydrogenase, 5,10-methylenetetrahydrofolate cyclohydrolase, 10-formyltetrahydrofolate synthetase

44



ATP5	M37104_at	M37104	PASS	9	11.44	PASS	12	9	7.42	1.54	1.54	ATP5	10	ATP synthase, H+ transporting, mitochondrial	ATP synthase, H+ transporting, mitochondrial
ATP6E	D49400_at	D49400	PASS	9	33.11	PASS	13	9	21.46	1.54	1.54	ATP6S14	12	ATPase, vacuolar, 14 kD	ATPase, vacuolar, 14 kD
TIS11D	U07802_at	U07802	PASS	9	37.56	PASS	13	9	24.38	1.54	1.54			Tis11d	similar to human PHAP12a encoded by GenBank Accession Number Y07569 and human PHAP12b encoded by GenBank Accession Number Y07570
U70439_s_at	U70439_s_at	U70439	PASS	9	87.67	PASS	13	9	56.92	1.54	1.54				silver-stainable protein SSP29
CIRBP	D78134_at	D78134	PASS	9	53.89	PASS	13	9	35.00	1.54	1.54	CIRBP	19p13.3	cold inducible RNA-binding protein	cold inducible RNA-binding protein
MAD2L1	U68018_at	U68018	PASS	7	9.00	PASS	13	7	5.85	1.54	1.54	hMAD-2		mad protein homolog	
RPL30	HG2873-HT3	HG2873-HT3	PASS	9	487.44	PASS	13	9	317.15	1.54	1.54	ATP5O	21q22.1-q22.2	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein)	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein)
ATP5O	X83218_at	X83218	PASS	9	22.44	PASS	13	9	14.62	1.54	1.54				
RPL26	HG384-HT38	HG384-HT38	PASS	9	170.56	PASS	13	9	111.08	1.54	1.54				match to X98253 (NID g2274981) (PID:g2274982)
AC002477_s_at	AC002477_s_at	AC002477	PASS	9	13.22	PASS	13	9	8.62	1.53	1.53	ZNF183		zinc-finger protein	
UBECS	U73379_at	U73379	PASS	5	9.20	PASS	10	5	6.00	1.53	1.53			cyclin-selective ubiquitin carrier protein	UbcH10
DEC	U49352_at	U49352	PASS	6	10.17	PASS	11	6	6.64	1.53	1.53	DEC	8q21.3	2,4-dienoyl CoA reductase	2,4-dienoyl CoA reductase
X55037_s_at	X55037_s_at	X55037	PASS	7	9.86	PASS	9	7	6.44	1.53	1.53	GATA3	10p15	GATA-binding protein 3	GATA-binding protein 3
IL8RB	L19593_at	L19593	PASS	5	7.80	PASS	10	5	5.10	1.53	1.53	IL8RB	2q35	interleukin 8 receptor, beta	interleukin 8 receptor, beta
TAF2D	U18062_at	U18062	PASS	9	8.67	PASS	12	9	5.67	1.53	1.53	TAF155		TFIID subunit TAF155	
DBI	M14200_ma	M14200	PASS	8	16.00	PASS	13	8	10.46	1.53	1.53	DBI			diazepam binding inhibitor
HG4264-HT4	HG4264-HT4	HG4264-HT4	PASS	9	14.11	PASS	13	9	9.23	1.53	1.53				
ACO2	U80040_at	U80040	PASS	8	13.75	PASS	13	8	9.00	1.53	1.53	ACO2	22q11.2-q13.31	aconitase 2, mitochondrial	aconitase 2, mitochondrial
H1AE	X56841_at	X56841	PASS	9	140.78	PASS	13	9	92.31	1.53	1.53	H1A-E			
NF2TS	HG3236-HT3	HG3236-HT3	PASS	9	44.22	PASS	13	9	29.00	1.52	1.52				
ACAT1	HG4073-HT4	HG4073-HT4	PASS	9	9.78	PASS	12	9	6.42	1.52	1.52				
S75256_s_at	S75256_s_at	S75256	PASS	8	10.25	PASS	11	8	6.73	1.52	1.52	HNL			neutrophil lipocalin
MNDA	M81750_at	M81750	PASS	8	41.13	PASS	13	8	27.00	1.52	1.52	MNDA	1q22	myeloid cell nuclear differentiation antigen	myeloid cell nuclear differentiation antigen
TCRB	M12886_at	M12886	PASS	9	227.67	PASS	13	9	149.69	1.52	1.52	TCRB	7q35	T-cell receptor, beta cluster	T-cell receptor, beta cluster
L09209_s_at	L09209_s_at	L09209	PASS	9	45.89	PASS	13	9	30.23	1.52	1.52	APLP2	11q23-q25	amyloid beta (A4) precursor-like protein 2	amyloid beta (A4) precursor-like protein 2
FTL	M11147_at	M11147	PASS	9	409.56	PASS	13	9	269.92	1.52	1.52	FTL	19q13.3-q13.4	ferritin, light polypeptide	ferritin, light polypeptide
ARD1	U14575_at	U14575	PASS	8	8.25	PASS	9	8	5.44	1.52	1.52	PPP1R8	Chr.1	protein phosphatase 1, regulatory (inhibitor) subunit 8	protein phosphatase 1, regulatory (inhibitor) subunit 8
H1A-A	M94880_f	M94880	PASS	9	275.11	PASS	13	9	181.69	1.51	1.51				
M19311_s_at	M19311_s_at	M19311	PASS	9	108.67	PASS	13	9	71.77	1.51	1.51				
M30448_s_at	M30448_s_at	M30448	PASS	9	58.11	PASS	13	9	38.38	1.51	1.51	CSNK2B	6p21-p12	casein kinase 2, beta polypeptide	casein kinase 2, beta polypeptide
BACTIN3	AFFX-HSAC	AFFX-HSAC	PASS	9	385.33	PASS	13	9	254.54	1.51	1.51				
M13560_s_at	M13560_s_at	M13560	PASS	9	150.33	PASS	13	9	99.31	1.51	1.51				
RPL38	Z26876_at	Z26876	PASS	9	308.11	PASS	13	9	203.62	1.51	1.51	RPL38	17	cell surface glycoprotein	la-associated gamma chain
CLIC1	U93205_at	U93205	PASS	9	94.22	PASS	13	9	62.31	1.51	1.51	CLIC1		chloride intracellular channel 1	ribosomal protein L38
NHC	U90549_at	U90549	PASS	5	12.40	PASS	10	5	8.20	1.51	1.51	NHC		non-histone chromosomal protein	chloride intracellular channel 1

NPAT	D83243_at	D83243	PASS	9	9.89	PASS	11	9	6.55	1.51	1.51	NPAT	11q22-q23	nuclear protein, ataxia-telangiectasia locus	nuclear protein, ataxia-telangiectasia locus
NRNP	M16342_at	M16342	PASS	9	25.44	PASS	13	9	16.85	1.51	1.51	HNRPC		heterogeneous nuclear ribonucleoprotein C (C1/C2)	heterogeneous nuclear ribonucleoprotein C (C1/C2)
HG1322-HT	HG1322-HT3	HG1322-HT3	PASS	9	49.22	PASS	13	9	32.62	1.51	1.51	SNCA	4q21.3-q22	synuclein, alpha (non A4 component of amyloid precursor)	synuclein, alpha (non A4 component of amyloid precursor)
SNCA	U46901_at	U46901	PASS	9	8.11	PASS	8	9	5.38	1.51	1.51	SNCA		synuclein, alpha (non A4 component of amyloid precursor)	synuclein, alpha (non A4 component of amyloid precursor)
K5	D13630_at	D13630	PASS	8	12.75	PASS	11	8	8.45	1.51	1.51	KIAA0005		KIAA0005 gene product	KIAA0005 gene product
HDAC1	D50405_at	D50405	PASS	9	16.22	PASS	13	9	10.77	1.51	1.51	HDAC1	Jp34.1	histone deacetylase 1	histone deacetylase 1
GJA4	Y08915_at	Y08915	PASS	9	19.11	PASS	13	9	12.69	1.51	1.51	IGBP1	Xq13.1-q13.3	immunoglobulin (CD79A) binding protein 1	immunoglobulin (CD79A) binding protein 1
LUCA15	U23946_at	U23946	PASS	6	9.33	PASS	10	6	6.20	1.51	1.51	LUCA15		putative tumor suppressor	putative tumor suppressor
VDAC2	L08666_at	L08666	PASS	9	19.89	PASS	13	9	13.23	1.50	1.50	VDAC2	10q22	voltage-dependent anion channel 2	voltage-dependent anion channel 2
M83667_ma	M83667_ma	M83667	PASS	9	42.67	PASS	13	9	28.38	1.50	1.50	NF-IL6-beta		NF-IL6-beta protein	NF-IL6-beta protein
CIH3	U57877_at	U57877	PASS	5	14.80	PASS	13	5	9.85	1.50	1.50	SDHC	1q21	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD
U89922_s_at	U89922_s_at	U89922	PASS	9	143.56	PASS	13	9	95.54	1.50	1.50	LTB	6p21.3	lymphotoxin beta (TNF superfamily, member 3)	lymphotoxin beta (TNF superfamily, member 3)
LYZ_ma1_f	X14008_ma	X14008	PASS	9	159.22	PASS	13	9	106.00	1.50	1.50			Protein sequence is in conflict with the conceptual translation	Protein sequence is in conflict with the conceptual translation
NDUFB2	M22538_at	M22538	PASS	8	28.88	PASS	13	8	19.23	1.50	1.50	NDUFB2	18p11.31-p11.2	NADH-ubiquinone reductase (ubiquinone) flavoprotein 2 (24kD)	NADH-ubiquinone reductase (ubiquinone) flavoprotein 2 (24kD)
I05072_s_at	I05072_s_at	I05072	PASS	9	17.56	PASS	13	9	11.69	1.50	1.50	IRF1	5q23-q31	interferon regulatory factor 1	interferon regulatory factor 1
K247	D87434_at	D87434	PASS	8	10.63	PASS	13	8	7.08	1.50	1.50	KIAA0247		KIAA0247 gene product	KIAA0247 gene product
RPS10	U14972_at	U14972	PASS	9	350.00	PASS	13	9	233.31	1.50	1.50	RPS10	6	ribosomal protein S10	ribosomal protein S10
NOT56L	Y09022_at	Y09022	PASS	8	12.13	PASS	12	8	8.08	1.50	1.50	not		Not56-like protein	Not56-like protein
BTG1	X61123_at	X61123	PASS	9	54.11	PASS	13	9	36.08	1.50	1.50	BTG1	12q22	B-cell translocation gene 1, anti-proliferative	B-cell translocation gene 1, anti-proliferative
HMOX1	X06985_at	X06985	PASS	8	32.63	PASS	13	8	21.77	1.50	1.50	HMOX1	22q12	heme oxygenase (decycling) 1	heme oxygenase (decycling) 1
RPS29	U14973_at	U14973	PASS	9	390.44	PASS	13	9	260.54	1.50	1.50	RPS29	14	ribosomal protein S29	ribosomal protein S29
PSMHSC7	D26599_at	D26599	PASS	9	24.22	PASS	12	9	16.17	1.50	1.50	PSMB2	1p34.2	proteasome (prosome, macropain) subunit, beta type, 2	proteasome (prosome, macropain) subunit, beta type, 2
SPTBN1	M96803_at	M96803	PASS	5	10.60	PASS	13	5	7.08	1.50	1.50	SPTBN1	2p21	spectrin, beta, non-erythrocytic 1	spectrin, beta, non-erythrocytic 1
K98_TCP1	D43950_at	D43950	PASS	8	17.63	PASS	13	8	11.77	1.50	1.50	KIAA0098		KIAA0098 is a human counterpart of mouse chaperonin containing TCP-1 gene.	KIAA0098 is a human counterpart of mouse chaperonin containing TCP-1 gene.
K137_COSC	D50927_at	D50927	PASS	8	10.25	PASS	13	8	6.85	1.50	1.50	KIAA0137		KIAA0137 gene product	KIAA0137 gene product
PAK1	U24152_at	U24152	PASS	9	13.22	PASS	12	9	8.83	1.50	1.50	PAK1	11q13-q14	p21/Cdc42/Rac1-activated kinase 1 (yeast Ste20-related)	p21/Cdc42/Rac1-activated kinase 1 (yeast Ste20-related)
U76764_s_at	U76764_s_at	U76764	PASS	9	38.67	PASS	13	9	25.85	1.50	1.50	CD97	19p13	CD97 antigen	CD97 antigen
X65965_s_at	X65965_s_at	X65965	PASS	9	19.44	PASS	13	9	13.00	1.50	1.50				

HCPA78L	S73591_s_at	S73591	PASS	9	350.56	PASS	13	9	234.46	1.50	1.50	brain-expressed HHCPA78 homolog			VDUP1	1,25-dihydroxyvitamin D-3 up-regulated; This sequence comes from Fig. 2. Protein sequence is in conflict with the conceptual translation; mismatch(26[k-&gt;R])
S79873_s_at	S79873_s_at	S79873	PASS	7	7.29	PASS	8	7	4.88	1.49	1.49	LAMP2	Xq24		lysosomal-associated membrane protein 2	lysosomal-associated membrane protein 2
L03411_s_at	L03411_s_at	L03411	PASS	9	10.00	PASS	13	9	6.69	1.49	1.49	RD	pter-p22.1		Radin blood group	Radin blood group
RPS27	HG3214-HT	HG3214-H	PASS	9	438.11	PASS	13	9	293.46	1.49	1.49	COX8	11q12-q13		cytochrome c oxidase subunit VIII	cytochrome c oxidase subunit VIII
COX8_ma1	J04823_ma1	J04823	PASS	9	80.33	PASS	13	9	53.85	1.49	1.49	KIAA0127	2q14-q21		glycophorin C (Gerbich blood group)	glycophorin C (Gerbich blood group)
K127	D50917_at	D50917	PASS	7	8.29	PASS	9	7	5.56	1.49	1.49	GYPC	11q13		chromosome 11 open reading frame 4	KIAA0127 gene product
M36284_s_at	M36284_s_at	M36284	PASS	9	28.33	PASS	13	9	19.00	1.49	1.49	C11orf4			proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11
NOF1	U39400_at	U39400	PASS	8	11.25	PASS	11	8	7.55	1.49	1.49	PSMD11			uridine diphosphoglucose pyrophosphorylase	uridine diphosphoglucose pyrophosphorylase
WTRP	HG3549-HT	HG3549-H	PASS	9	410.22	PASS	13	9	275.23	1.49	1.49				transcriptional coactivator p52/p75	transcriptional coactivator p52/p75
NELRP2	D83018_at	D83018	PASS	9	18.22	PASS	13	9	12.23	1.49	1.49				unc119 (C.elegans) homolog	unc119 (C.elegans) homolog
PSM445	AB003102_at	AB003102	PASS	7	13.57	PASS	9	7	9.11	1.49	1.49				Tu translation elongation factor, mitochondrial	Tu translation elongation factor, mitochondrial
UDPPH	U27460_at	U27460	PASS	9	12.22	PASS	9	9	8.22	1.49	1.49				ribosomal protein L18	ribosomal protein L18
DPS70	U94319_at	U94319	PASS	9	12.00	PASS	13	9	8.08	1.49	1.49				ATP synthase, H <sup>+</sup> -transporting, mitochondrial F1 complex, alpha subunit, isoform 1, cardiac muscle	ATP synthase, H <sup>+</sup> -transporting, mitochondrial F1 complex, alpha subunit, isoform 1, cardiac muscle
HRG4	U40998_at	U40998	PASS	8	11.75	PASS	12	8	7.92	1.48	1.48				transcriptional coactivator p52/p75	transcriptional coactivator p52/p75
P43LSB	S75463_at	S75463	PASS	9	29.11	PASS	13	9	19.62	1.48	1.48				Tu translation elongation factor, mitochondrial	Tu translation elongation factor, mitochondrial
RPL18AH	L11566_at	L11566	PASS	9	309.00	PASS	13	9	208.23	1.48	1.48				ribosomal protein L18	ribosomal protein L18
ATPA	D14710_at	D14710	PASS	9	90.22	PASS	13	9	60.85	1.48	1.48				ATP synthase, H <sup>+</sup> -transporting, mitochondrial F1 complex, alpha subunit, isoform 1, cardiac muscle	ATP synthase, H <sup>+</sup> -transporting, mitochondrial F1 complex, alpha subunit, isoform 1, cardiac muscle
K261_SIS	D87450_at	D87450	PASS	9	8.67	PASS	13	9	5.85	1.48	1.48				Similar to D-melanogaster parallel sister chromatids protein	Similar to D-melanogaster parallel sister chromatids protein
HBC647	U68494_at	U68494	PASS	7	8.00	PASS	10	7	5.40	1.48	1.48				ORF1	ORF1
OAZ	D78361_at	D78361	PASS	9	383.22	PASS	13	9	258.69	1.48	1.48				ribosomal protein L32	ribosomal protein L32
RPL32	X03342_at	X03342	PASS	9	420.11	PASS	13	9	283.85	1.48	1.48				interferon gamma receptor 1	interferon gamma receptor 1
U19247_ma1	U19247_ma1	U19247	PASS	9	14.11	PASS	13	9	9.54	1.48	1.48				special AT-rich sequence binding protein 1 (binds to nuclear matrix/scaffold-DNA's)	special AT-rich sequence binding protein 1 (binds to nuclear matrix/scaffold-DNA's)
SATB1	M97287_at	M97287	PASS	9	19.78	PASS	13	9	13.38	1.48	1.48				associating DNA's) unknown protein	associating DNA's) unknown protein
CIT987SK_f	U96629_ma1	U96629	PASS	8	8.13	PASS	8	8	5.50	1.48	1.48				CIT987SK_2A8_1	CIT987SK_2A8_1
HG1471-HT	HG1471-HT	HG1471-H	PASS	7	7.71	PASS	9	7	5.22	1.48	1.48					

CD48	M37766_at	M37766	PASS	9	121.67	PASS	13	9	82.38	1.48	1.48	CD48	lq21.3-q22	CD48 antigen (B-cell membrane protein)
HNRPAL	mX12671	maX12671	PASS	9	87.11	PASS	13	9	59.00	1.48	1.48	hump a1 protein		
UBE2N	D83004_at	D83004	PASS	9	9.89	PASS	10	9	6.70	1.48	1.48	ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13)		ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13)
GTF2A2	U14193_at	U14193	PASS	8	11.13	PASS	13	8	7.54	1.48	1.48	GTF2A1		general transcription factor IIA, 1 (37kD and 19kD subunits)
TI227H	D50525_at	D50525	PASS	9	9.44	PASS	10	9	6.40	1.48	1.48			highly similar to UDP-N-acetylglucosamine transporter of K. lactis
UGALT	D87989_at	D87989	PASS	7	13.14	PASS	11	7	8.91	1.48	1.48	UGTrel1		
SAP145	U41371_at	U41371	PASS	9	17.78	PASS	11	9	12.09	1.47	1.47	SAP 145		spliceosome associated protein
CMKRL1	U20350_at	U20350	PASS	9	63.78	PASS	13	9	43.38	1.47	1.47	CX3CR1	3p21	chemokine (C-X3-C) receptor 1
RPL27	L19527_at	L19527	PASS	9	320.89	PASS	13	9	218.31	1.47	1.47	RPL27	17	ribosomal protein L27
SPTAN1	J05243_at	J05243	PASS	8	8.00	PASS	9	8	5.44	1.47	1.47	SPTAN1	9q33-q34	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)
G22P1	M30938_at	M30938	PASS	9	19.78	PASS	13	9	13.46	1.47	1.47			Ku (p70/p80) subunit
MCP	X59405_at	X59405	PASS	8	9.38	PASS	13	8	6.38	1.47	1.47			
K264	D87453_at	D87453	PASS	5	7.60	PASS	11	5	5.18	1.47	1.47	KIAA0264		
SRP14	U07857_at	U07857	PASS	9	47.78	PASS	13	9	32.62	1.46	1.46	SRP14	15q22	signal recognition particle (homologous to RNA-binding protein)
K111_NUK3	D21853_at	D21853	PASS	9	16.00	PASS	13	9	10.92	1.46	1.46	KIAA0111		KIAA0111 gene product
IFI27SEP	J04164_at	J04164	PASS	9	227.56	PASS	13	9	155.38	1.46	1.46	IFI17		interferon-induced protein 17
RPL35	U12465_at	U12465	PASS	9	268.44	PASS	13	9	183.31	1.46	1.46			ribosomal protein L35
CCT6	L27706_at	L27706	PASS	7	9.57	PASS	13	7	6.54	1.46	1.46	CCT6		chaperonin containing T-complex subunit 6
FNTA	L10413_at	L10413	PASS	9	34.33	PASS	13	9	23.46	1.46	1.46			farnesyl-protein transferase alpha-subunit
RPS9	U14971_at	U14971	PASS	9	277.78	PASS	13	9	189.85	1.46	1.46	RPS9	19q13.4	ribosomal protein S9
U09510_s at	U09510_s at	U09510	PASS	9	8.33	PASS	10	9	5.70	1.46	1.46	GARS	7p15	glycyl-tRNA synthetase
PECAM1	L34657_at	L34657	PASS	8	18.75	PASS	12	8	12.83	1.46	1.46	PECAM1	17q23	platelet/endothelial cell adhesion molecule (CD31 antigen)
NPC1	AF002020_at	AF002020	PASS	5	8.60	PASS	9	5	5.89	1.46	1.46	NPC1	18	Niemann-Pick disease, type C1
HSP40	D85429_at	D85429	PASS	9	21.89	PASS	13	9	15.00	1.46	1.46	HSPF1		Hsp40; Similar to bacterial DnaJ heat shock protein
PPP3CB	S46622_at	S46622	PASS	5	6.40	PASS	10	5	4.40	1.45	1.45	calcineurin A catalytic subunit		This sequence comes from Fig. 1; calmodulin-dependent protein phosphatase catalytic subunit; CaM-PrP catalytic subunit
ZPK	U07358_at	U07358	PASS	7	8.86	PASS	11	7	6.09	1.45	1.45	ZPK	12q13	zipper (leucine) protein kinase
RPL12	L06505_at	L06505	PASS	9	221.67	PASS	13	9	152.46	1.45	1.45	RPL12		ribosomal protein L12
MMP1	M63483_at	M63483	PASS	5	12.60	PASS	12	5	8.67	1.45	1.45			ribosomal protein L12

U45328_s_at	U45328_s_at	U45328	PASS	6	16.33	PASS	12	6	11.25	1.45	1.45	1.45	16p13.3	ubiquitin-conjugating enzyme E21 (homologous to yeast UBC9)
ACTN1	M95178_at	M95178	PASS	7	12.71	PASS	13	7	8.77	1.45	1.45	1.45	14q24	actinin, alpha 1
SFR54	L14076_at	L14076	PASS	9	11.11	PASS	12	9	7.67	1.45	1.45	1.45		SR protein family member, SR domain: (bp 583..1529); RNA binding domains: RNP-2 (bp 57..80) and RNP-1 (bp 150..173)
D12775_s_at	D12775_s_at	D12775	PASS	9	7.11	PASS	11	9	4.91	1.45	1.45	1.45	11pter-p13	adenosine monophosphate deaminase (isoform E)
PF4V1_ma1	M26167_ma	M26167	PASS	6	7.50	PASS	11	6	5.18	1.45	1.45	1.45		precursor protein
ANX4	M82809_at	M82809	PASS	6	7.83	PASS	12	6	5.42	1.45	1.45	1.45	2p13	annexin IV (placental anticoagulant protein II)
RPL37	HG3364-HT3	HG3364-H	PASS	9	405.56	PASS	13	9	280.62	1.45	1.45	1.45		Protein sequence is in conflict with the conceptual translation.
HLADRA	X00274_at	X00274	PASS	9	327.33	PASS	13	9	226.54	1.44	1.44	1.44		similar to chicken alpha2 isoform
CAPZA	U03851_at	U03851	PASS	9	21.56	PASS	13	9	14.92	1.44	1.44	1.44		integrin, beta 7
CMPSIAT	D87969_at	D87969	PASS	9	10.11	PASS	12	9	7.00	1.44	1.44	1.44	12q13.1	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2
ITGB7	S80335_at	S80335	PASS	9	16.44	PASS	13	9	11.38	1.44	1.44	1.44	12q23-q24.1	beta-2 microglobulin
ATP2A2	M23114_at	M23114	PASS	5	6.60	PASS	7	5	4.57	1.44	1.44	1.44		proteasome (prosome, macropain) subunit, beta type, 10
J00105_s_at	J00105_s_at	J00105	PASS	9	422.56	PASS	13	9	292.69	1.44	1.44	1.44	16q22.1	CASP8 and FADD-like apoptosis regulator
PSMB10_cds	X71874_cds	X71874	PASS	9	73.89	PASS	13	9	51.23	1.44	1.44	1.44		translocated promoter region (to activated MET oncogene)
CLARP	AF005775_at	AF005775	PASS	8	9.00	PASS	12	8	6.25	1.44	1.44	1.44	2q33-q34	pre-mRNA processing factor
NTRK1	X66397_at	X66397	PASS	9	15.22	PASS	12	9	10.58	1.44	1.44	1.44	1	ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide
TRA2A	U53209_at	U53209	PASS	7	22.14	PASS	10	7	15.40	1.44	1.44	1.44		guanine nucleotide binding protein (G protein), beta polypeptide 1
ATP5B	M19483_at	M19483	PASS	9	46.22	PASS	13	9	32.15	1.44	1.44	1.44	12p13-qter	reading frame (part 8) (1 is 2nd base in codon)
RPL30	HG311-HT3	HG311-H	PASS	9	202.44	PASS	13	9	140.85	1.44	1.44	1.44		ribosomal protein L23
M36430_s_at	M36430_s_at	M36430	PASS	7	12.71	PASS	13	7	8.85	1.44	1.44	1.44	1p36.21-36.33	ribosomal protein L4
IGHMBP2	V00563_at	V00563	PASS	9	42.56	PASS	13	9	29.62	1.44	1.44	1.44		ribosomal protein L4
RPL17	X55954_at	X55954	PASS	9	294.00	PASS	13	9	204.69	1.44	1.44	1.44	17q	zinc finger protein 134 (clone pHZ-15)
RPL4	D23660_at	D23660	PASS	9	297.78	PASS	13	9	207.46	1.44	1.44	1.44	15	ATPase, Na+/K+ transporting, beta 3 polypeptide
D63861_s_at	D63861_s_at	D63861	PASS	7	7.71	PASS	8	7	5.38	1.44	1.44	1.44		synactin 4A (placental)
ZNF134	U09412_at	U09412	PASS	7	6.86	PASS	9	7	4.78	1.44	1.44	1.44	19q13.4	luteal phase endometrial protein 1
ATP1B3	U51478_at	U51478	PASS	9	32.11	PASS	13	9	22.38	1.43	1.43	1.43	3q22-q23	homologue
STX4A	U07158_at	U07158	PASS	9	11.22	PASS	12	9	7.83	1.43	1.43	1.43		CD3Z antigen, zeta polypeptide (TIT3 complex)
HO3	U18937_at	U18937	PASS	8	7.88	PASS	10	8	5.50	1.43	1.43	1.43		
CD3Z	J04132_at	J04132	PASS	9	31.56	PASS	13	9	22.08	1.43	1.43	1.43	1q22-q25	
K41_ZNF62	D26069_at	D26069	PASS	7	8.43	PASS	10	7	5.90	1.43	1.43	1.43		

CD79B	M89957_at	M89957	PASS	6	12.33	PASS	11	6	8.64	1.43	1.43	CD79B	17q23	cell surface glycoprotein	CD79B antigen (immunoglobulin-associated beta)
UQCRLS1	L32977_at	L32977	PASS	9	27.22	PASS	13	9	19.08	1.43	1.43	UQCRLS1		Rieske Fe-S protein	phosphate carrier, mitochondrial
PHC	X60036_at	X60036	PASS	9	57.89	PASS	13	9	40.62	1.43	1.43	PHC	12	phosphate carrier, mitochondrial	ribosomal protein S16
RPS16	M60854_at	M60854	PASS	9	411.67	PASS	13	9	289.15	1.42	1.42	RPS16	19q	ribosomal protein S16	thymosin, beta 4, Y chromosome
TMSB4	M17733_at	M17733	PASS	9	430.44	PASS	13	9	302.69	1.42	1.42	TMSB4Y	Y	thymosin, beta 4, Y chromosome	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (hydroxymethylglutaricaciduria)
HMGCL	L07033_at	L07033	PASS	8	7.75	PASS	11	8	5.45	1.42	1.42	HMGCL	1	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (hydroxymethylglutaricaciduria)	ribosomal protein S6 kinase, 90kD, polypeptide 3
RPS6KA2	U08316_at	U08316	PASS	5	8.00	PASS	11	5	5.64	1.42	1.42	RPS6KA3	Xp22.2-p22.1	ribosomal protein S6 kinase, 90kD, polypeptide 3	growth factor receptor-bound protein 2
M96995_s_a	M96995_s_a	M96995	PASS	6	18.00	PASS	13	6	12.69	1.42	1.42	GIRB2	17q24-q25	growth factor receptor-bound protein 2	37L RP/p40, metastasis-associated multifunctional protein
U43901_ma	U43901_ma	U43901	PASS	9	287.89	PASS	13	9	203.08	1.42	1.42			37 kD laminin receptor precursor/p40 ribosome associated protein	ribosomal protein L37a
RPL37A	L06499_at	L06499	PASS	9	428.44	PASS	13	9	302.38	1.42	1.42	RPL37A		ribosomal protein L37a	similar to yeast YCR032w, GenBank Accession Number X59720, Mus musculus BG, GenBank Accession Number U52461 and C. elegans F10F2.1, GenBank Accession Number Z35598; previously identified as CDC4L
GILB1	M83822_at	M83822	PASS	7	7.43	PASS	12	7	5.25	1.41	1.41	BGL		beige-like protein	coagulation factor XIII, A1 polypeptide
F13A1	M14539_at	M14539	PASS	9	78.00	PASS	13	9	55.15	1.41	1.41	F13A1	6p24.2-p23	coagulation factor XIII, A1 polypeptide	prothymosin alpha
M26708_s_a	M26708_s_a	M26708	PASS	9	183.67	PASS	13	9	130.00	1.41	1.41	PTMA		T-cell receptor, alpha (V.D.J.C)	ribosomal protein S15a
K02777_s_at	K02777_s_at	K02777	PASS	7	25.86	PASS	13	7	18.31	1.41	1.41	TCRA	14q11.2	T-cell receptor, alpha (V.D.J.C)	apoptosis inhibitor 2
ITRAF	U59863_at	U59863	PASS	6	6.67	PASS	11	6	4.73	1.41	1.41			I-TRAF	ribosomal protein S15a
RPS24L	X62691_at	X62691	PASS	9	325.00	PASS	13	9	230.46	1.41	1.41	RPS15A	16p	ribosomal protein S15a	apoptosis inhibitor 2
MIHB	U37547_at	U37547	PASS	7	9.71	PASS	9	7	6.89	1.41	1.41	API2	11q22	apoptosis inhibitor 2	splicing factor, arginine/serine-rich (transformer 2 Drosophila homolog) 10
TRA2B	U68063_at	U68063	PASS	8	13.13	PASS	13	8	9.31	1.41	1.41	SFRS10	3q	splicing factor, arginine/serine-rich (transformer 2 Drosophila homolog) 10	RNA Polymerase II subunit 14.4 kD
POLR2F	Z27113_at	Z27113	PASS	9	22.33	PASS	13	9	15.85	1.41	1.41			RNA Polymerase II subunit 14.4 kD	ribosomal protein L8
RPL8	Z28407_at	Z28407	PASS	9	324.56	PASS	13	9	230.46	1.41	1.41	RPL8	8	ribosomal protein L8	differentiation 6 (deoxyguanosine triphosphate triphosphohydrolase)
K158_DIFP6	D63878_at	D63878	PASS	8	34.13	PASS	12	8	24.25	1.41	1.41	DIFP6	2q37	differentiation 6 (deoxyguanosine triphosphate triphosphohydrolase)	transcription factor ISGF-3
M97935_s_a	M97935_s_a	M97935	PASS	9	20.44	PASS	13	9	14.54	1.41	1.41			transcription factor ISGF-3	numb (Drosophila) homolog
SI71	L40393_at	L40393	PASS	8	8.25	PASS	8	8	5.88	1.40	1.40	NUMB	14q24.3	numb (Drosophila) homolog	KIAA0171 gene product
HG3638-HT	HG3638-HT	HG3638-H	PASS	5	9.20	PASS	9	5	6.56	1.40	1.40				pleckstrin homology, Sec7 and coiled/coil domains 1 (cytohesin 1)
K171_HYPL	D79993_at	D79993	PASS	6	7.83	PASS	12	6	5.58	1.40	1.40	KIAA0171		pleckstrin homology, Sec7 and coiled/coil domains 1 (cytohesin 1)	poly(carboxypeptidase (angiotensinase C))
YSEC7	M85169_at	M85169	PASS	9	22.56	PASS	13	9	16.08	1.40	1.40	PSCD1	17q25	pleckstrin homology, Sec7 and coiled/coil domains 1 (cytohesin 1)	
PRCP	L13977_at	L13977	PASS	9	14.67	PASS	11	9	10.45	1.40	1.40	PRCP	11q14	poly(carboxypeptidase (angiotensinase C))	

Map	L03532_at	L03532	PASS	9	25.89	PASS	13	9	18.46	1.40	1.40	1.40	ARC41	M4 protein p41-Arc	WD repeat containing protein; similar to Sop2Hs; 41 kD subunit of the Arp2/3 protein complex
ARC41	AF006084_at	AF006084	PASS	9	88.22	PASS	13	9	62.92	1.40	1.40	1.40			
K159	CHR1	D63880_at	D63880	PASS	8	7.00	PASS	9	5.00	1.40	1.40	1.40	KIAA0159		KIAA0159 gene product
E_POV2	U18919_at	U18919	PASS	5	6.80	PASS	7	5	4.86	1.40	1.40	1.40			
AQP3	AB001325_at	AB001325	PASS	9	20.56	PASS	13	9	14.69	1.40	1.40	1.40	AQP3	aquaporin 3	
ATP5G3	U09813_at	U09813	PASS	9	33.44	PASS	13	9	23.92	1.40	1.40	1.40	P3	mitochondrial ATP synthase subunit 9 precursor	
STAT3	L29277_at	L29277	PASS	8	10.13	PASS	12	8	7.25	1.40	1.40	1.40	STAT3	signal transducer and activator of transcription 3 (acute-phase response factor)	signal transducer and activator of transcription 3 (acute-phase response factor)
CSE1	U33286_at	U33286	PASS	8	8.75	PASS	11	8	6.27	1.39	1.39	1.39	CSE1L	chromosome segregation 1 (yeast homolog)-like	chromosome segregation 1 (yeast homolog)-like
HNRPG	Z23064_at	Z23064	PASS	9	12.33	PASS	13	9	8.85	1.39	1.39	1.39	HNRPG	heterogeneous nuclear ribonucleoprotein G	heterogeneous nuclear ribonucleoprotein G
U61397_s at	U61397_s at	U61397	PASS	9	9.22	PASS	13	9	6.62	1.39	1.39	1.39	UBL1	ubiquitin-like 1 (sentrim)	ubiquitin-like 1 (sentrim)
CD53	M37033_at	M37033	PASS	9	103.22	PASS	13	9	74.08	1.39	1.39	1.39	CD53	CD53 glycoprotein	CD53 antigen
RPL7A	M36072_at	M36072	PASS	9	272.56	PASS	13	9	195.62	1.39	1.39	1.39	RPL7A	ribosomal protein L7a	ribosomal protein L7a
ATP7A	AB000409_at	AB000409	PASS	9	9.89	PASS	10	9	7.10	1.39	1.39	1.39	MKNK1	MAP kinase-interacting serine/threonine kinase 1	MAP kinase-interacting serine/threonine kinase 1
RPS8_ma1	X67247_ma1	X67247	PASS	9	359.78	PASS	13	9	258.46	1.39	1.39	1.39	RPS8	ribosomal protein S8	ribosomal protein S8
K184	D80006_at	D80006	PASS	9	20.44	PASS	13	9	14.69	1.39	1.39	1.39	KIAA0184	ribosomal protein L6	ribosomal protein L6
RPL6	X69391_at	X69391	PASS	9	178.33	PASS	13	9	128.23	1.39	1.39	1.39	RPL6	p62	
SHGC	M88108_at	M88108	PASS	9	22.44	PASS	13	9	16.15	1.39	1.39	1.39	p62		
K107	D14663_at	D14663	PASS	7	11.86	PASS	13	7	8.54	1.39	1.39	1.39	KIAA0107	eukaryotic translation initiation factor 3, subunit 8 (110kD)	KIAA0107 gene product
EIF3	U46025_at	U46025	PASS	9	38.33	PASS	13	9	27.62	1.39	1.39	1.39	EIF388		eukaryotic translation initiation factor 3, subunit 8 (110kD)
K64	D31764_at	D31764	PASS	5	14.20	PASS	13	5	10.23	1.39	1.39	1.39	KIAA0064	protein tyrosine phosphatase, non-receptor type 12	KIAA0064 gene product
PTPN12	M93425_at	M93425	PASS	9	16.22	PASS	13	9	11.69	1.39	1.39	1.39	PTPN12	N-acylsphingosine amidohydrolase	protein tyrosine phosphatase, non-receptor type 12
ACERA	U70063_at	U70063	PASS	7	13.71	PASS	9	7	9.89	1.39	1.39	1.39	ASAH		N-acylsphingosine amidohydrolase
RPL5	HG4319-HT4HG4319-H	HG4319-HT4HG4319-H	PASS	9	351.78	PASS	13	9	253.69	1.39	1.39	1.39			
ATPBPCD	D64158_at	D64158	PASS	7	8.57	PASS	11	7	6.18	1.39	1.39	1.39		ATP binding protein	APACD-ATP binding protein associated with cell differentiation
SI00A10	M38591_at	M38591	PASS	9	75.56	PASS	13	9	54.54	1.39	1.39	1.39	SI00A10	SI00 calcium-binding protein A10 (annexin II ligand, calpactin I, light polypeptide)	SI00 calcium-binding protein A10 (annexin II ligand, calpactin I, light polypeptide)
GP25L2	X90872_at	X90872	PASS	8	15.13	PASS	13	8	10.92	1.38	1.38	1.38	gp25l2		associated to Golgi apparatus
K225_COSK	D86978_at	D86978	PASS	8	8.00	PASS	9	8	5.78	1.38	1.38	1.38	KIAA0225		similar to a C.elegans protein encoded in cosmid K12D12(Z49069)
SLC20A1	L20859_at	L20859	PASS	9	7.89	PASS	10	9	5.70	1.38	1.38	1.38	GLVR1	leukemia virus receptor 1	
U79528_s at	U79528_s at	U79528	PASS	9	15.00	PASS	13	9	10.85	1.38	1.38	1.38	SR31747	SR31747 binding protein 1	sterol isomerase 1; SR-BP1
RPS5	U14970_at	U14970	PASS	9	293.11	PASS	13	9	212.00	1.38	1.38	1.38	RP55	ribosomal protein S5	ribosomal protein S5
AFFX-HSAC	AFFX-HSAC	AFFX-HSAC	PASS	7	19.14	PASS	13	7	13.85	1.38	1.38	1.38			
MCM7	D55716_at	D55716	PASS	6	9.50	PASS	8	6	6.88	1.38	1.38	1.38	P1cdc47		
PBP1	U83463_at	U83463	PASS	8	10.63	PASS	13	8	7.69	1.38	1.38	1.38		scaffold protein Pbp1	

MDCR	U72342_at	U72342	PASS	9	12.11	PASS	13	9	8.77	1.38	1.38	1.38	PAFAH1B1	17p13.3-p13.3	platelet-activating factor acetylhydrolase, isoform 1b, alpha subunit (45kD)	platelet-activating factor acetylhydrolase, isoform 1b, alpha subunit (45kD)
RPI	L35035_at	L35035	PASS	8	7.25	PASS	8	8	5.25	1.38	1.38	1.38	UBE2D3		ubiquitin-conjugating enzyme E2D 3 (homologous to yeast UBC4/5)	ubiquitin-conjugating enzyme E2D 3 (homologous to yeast UBC4/5)
DDX	U90426_at	U90426	PASS	9	11.67	PASS	13	9	8.46	1.38	1.38	1.38			DEAD-box family member; contains DEAD-box, similar to rat liver nuclear protein p47 (PIR Accession Number A42881) and D. melanogaster DEAD-box RNA helicase WM6 (PIR Accession Number S51601)	DEAD-box family member; contains DEAD-box, similar to rat liver nuclear protein p47 (PIR Accession Number A42881) and D. melanogaster DEAD-box RNA helicase WM6 (PIR Accession Number S51601)
RPS25	M64716_at	M64716	PASS	9	275.67	PASS	13	9	200.15	1.38	1.38	1.38	RPS25	11q23.3	ribosomal protein S25	ribosomal protein S25
PSMB8	Z14982_mal	Z14982	PASS	8	30.75	PASS	12	8	22.33	1.38	1.38	1.38	MHC- encoded proteasome subunit		proteasome subunit LAMP7	alternative splicing
HG3730-HT4																
RPL21	U25789_at	U25789	PASS	8	9.75	PASS	12	8	7.08	1.38	1.38	1.38	RPL21	13	ribosomal protein L21	ribosomal protein L21
DUT	U31930_at	U31930	PASS	9	11.11	PASS	13	9	111.77	1.38	1.38	1.38	DUT	15q15-q21.1	dUTP pyrophosphatase	dUTP pyrophosphatase
EIF4G2	D86549_at	D86549	PASS	8	6.88	PASS	11	8	5.00	1.38	1.38	1.38			p97 homologous protein	
K232	D86985_at	D86985	PASS	6	7.00	PASS	11	6	5.09	1.38	1.38	1.38	KIAA0232		phosphogluconate dehydrogenase	KIAA0232 gene product
PGD	U30255_at	U30255	PASS	6	22.00	PASS	10	6	16.00	1.38	1.38	1.38	PGD	1p36.3-p36.13	phosphogluconate dehydrogenase	phosphogluconate dehydrogenase
EMAPII	U10117_at	U10117	PASS	9	10.11	PASS	11	9	7.36	1.37	1.37	1.37	EMAPII		endothelial-monocyte activating polypeptide II	endothelial-monocyte activating polypeptide
DSS1	U41515_at	U41515	PASS	9	8.78	PASS	10	9	6.40	1.37	1.37	1.37	DSS1			Method: conceptual translation supplied by author.
M14199_s_at	M14199_s_at	M14199	PASS	9	302.00	PASS	13	9	220.23	1.37	1.37	1.37	LAMR1	3p21.3	laminin receptor 1 (67kD); Ribosomal protein SA	laminin receptor 1 (67kD); Ribosomal protein SA
STXB3	D63506_at	D63506	PASS	9	10.33	PASS	13	9	7.54	1.37	1.37	1.37	Munc-18-3		non-metastatic cells 1, protein	non-metastatic cells 1, protein
NME1	X17620_at	X17620	PASS	8	8.38	PASS	9	8	6.11	1.37	1.37	1.37	NME1	17q22	non-metastatic cells 1, protein (NM23A) expressed in	(NM23A) expressed in
RPL3	X73460_at	X73460	PASS	9	364.22	PASS	13	9	265.77	1.37	1.37	1.37	RPL3	22	ribosomal protein L3	ribosomal protein L3
APEX	D13370_at	D13370	PASS	9	20.44	PASS	13	9	14.92	1.37	1.37	1.37	APEX	14q11.2-q12	APEX nuclease (multifunctional DNA repair enzyme)	APEX nuclease (multifunctional DNA repair enzyme)
K201	HSP10	D86956_at	PASS	6	7.00	PASS	9	6	5.11	1.37	1.37	1.37	KIAA0201		KIAA0201 gene product	KIAA0201 gene product
COX10	U82010_mal	U82010	PASS	9	8.56	PASS	12	9	6.25	1.37	1.37	1.37	COX10	17p12-p11.2	cytochrome c oxidase subunit X (theme A)	cytochrome c oxidase subunit X (theme A; farnesyltransferase)
LYZ_f	M19045_f_at	M19045	PASS	9	155.67	PASS	13	9	113.77	1.37	1.37	1.37	LYZ		lysosome precursor (EC 3.2.1.17)	lysosome precursor (EC 3.2.1.17)
RPL19	X63527_at	X63527	PASS	9	379.44	PASS	13	9	277.54	1.37	1.37	1.37	RPL19	17p12-q11	ribosomal protein L19	ribosomal protein L19
DPYD	U20938_at	U20938	PASS	8	9.25	PASS	13	8	6.77	1.37	1.37	1.37			dihydropyrimidine dehydrogenase	DPD; dihydropyrimidine dehydrogenase
Z47055_s_at	Z47055_s_at	Z47055	PASS	9	9.22	PASS	12	9	6.75	1.37	1.37	1.37	FDP5		farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase)	farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase)



LYN	M16038_at	M16038	PASS	9	17.11	PASS	13	9	12.54	1.36	1.36	LYN	8q13	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog
hum alu at	hum alu at	PASS		9	422.44	PASS	13	9	309.62	1.36	1.36				
PCM1	L27841_at	PASS		6	7.83	PASS	8	6	5.75	1.36	1.36	PCM-1		pericentriol material 1	
ACAA	D16294_at	PASS		8	9.13	PASS	10	8	6.70	1.36	1.36			mitochondrial 3-oxoacyl-CoA thiolase	
PSMA3	D00760_at	PASS		8	11.00	PASS	12	8	8.08	1.36	1.36	PSMA2	6q27	proteasome (prosome, macropain) subunit, alpha type, 2	proteasome (prosome, macropain) subunit, alpha type, 2
U07806_s_at	U07806_s_at	PASS		8	11.25	PASS	11	8	8.27	1.36	1.36			DNA topoisomerase I	found in the camptothecin resistant clone CEM/C2
A82KD	U15552_at	PASS		7	8.71	PASS	12	7	6.42	1.36	1.36			acidic 82 kDa protein	
D26535_s_at	D26535_s_at	PASS		8	10.00	PASS	11	8	7.36	1.36	1.36	DLST	14q24.3	dihydroliponamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	dihydroliponamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)
Z49148_s_at	Z49148_s_at	PASS		9	285.33	PASS	13	9	210.23	1.36	1.36	RPL29	3q29-qter	ribosomal protein L29	ribosomal protein L29
EED	U90651_at	PASS		7	8.14	PASS	11	7	6.00	1.36	1.36	EED	11q14.2-q22.3	embryonic ectoderm development protein	embryonic ectoderm development protein
DYRK2	Y09216_at	PASS		6	10.17	PASS	12	6	7.50	1.36	1.36	DYRK2	12	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2
LLREP3	X17206_at	PASS		9	471.00	PASS	13	9	347.46	1.36	1.36	RPS2	16p13.3	ribosomal protein S2	ribosomal protein S2
UBA52_ma1	X56997_ma1	PASS		9	268.44	PASS	13	9	198.08	1.36	1.36	UBA52		ubiquitin-52 amino acid fusion protein	
RPS18	X69150_at	PASS		9	377.78	PASS	13	9	278.77	1.36	1.36	RPS18	6p21.3	ribosomal protein S18	ribosomal protein S18
FCER2	M15059_at	PASS		9	9.33	PASS	9	9	6.89	1.35	1.35	FCER2	19p13.3	Fc fragment of IgE, low affinity II, receptor for (CD23A)	Fc fragment of IgE, low affinity II, receptor for (CD23A)
P87	L42572_at	PASS		8	8.38	PASS	11	8	6.18	1.35	1.35	p87/89		transmembrane protein	transmembrane protein
BTX_ma4	U78027_ma4	PASS		7	10.71	PASS	12	7	7.92	1.35	1.35	FTP3		FTP3	lysosomal exoglycosidase
HCG8	X92110_at	PASS		5	5.80	PASS	7	5	4.29	1.35	1.35				
PSKH1	U09564_at	PASS		8	7.50	PASS	11	8	5.55	1.35	1.35	SRPK1	6p21.2-p21.3	SFRS protein kinase 1	SFRS protein kinase 1
U09820_s_at	U09820_s_at	PASS		7	8.71	PASS	9	7	6.44	1.35	1.35	ATRXL	Xq13.1-q21.1	alpha thalassemia/mental retardation syndrome X-linked	alpha thalassemia/mental retardation syndrome X-linked
U37546_s_at	U37546_s_at	PASS		8	7.13	PASS	11	8	5.27	1.35	1.35	APII	11q22	apoptosis inhibitor 1	apoptosis inhibitor 1
S54005_s_at	S54005_s_at	PASS		9	184.44	PASS	13	9	136.54	1.35	1.35	thymosin beta-10		thymosin beta-10	This sequence comes from Fig. 1.
LKYHYD	U57721_at	PASS		9	9.44	PASS	13	9	7.00	1.35	1.35	KYNUL		kynureninase; L-kynurenine hydrolase	kynureninase; L-kynurenine hydrolase
X95325_s_at	X95325_s_at	PASS		5	21.80	PASS	12	5	16.17	1.35	1.35	dbpav		variant A	variant A
RARS	S80343_at	PASS		8	7.50	PASS	7	8	5.57	1.35	1.35	RARS	5pter-q11	arginyl-tRNA synthetase	arginyl-tRNA synthetase
K148	D63482_at	PASS		5	7.80	PASS	10	5	5.80	1.34	1.34	KIAA0148		KIAA0148 gene product	KIAA0148 gene product
K178_SMC1	D80000_at	PASS		6	6.17	PASS	10	6	4.60	1.34	1.34	KIAA0178		similar to mitosis-specific chromosome segregation protein SMC1 of S.cerevisiae	similar to mitosis-specific chromosome segregation protein SMC1 of S.cerevisiae
RPS11	X06617_at	PASS		9	380.22	PASS	13	9	284.08	1.34	1.34	RPS11	19q13.3	ribosomal protein S11	ribosomal protein S11
JUN	U65928_at	PASS		8	8.75	PASS	11	8	6.55	1.34	1.34	JUN	1p32-p31	Avian sarcoma virus 17 (v-jun) oncogene homolog	v-jun avian sarcoma virus 17 oncogene homolog
INT6	U62962_at	PASS		9	52.67	PASS	13	9	39.46	1.33	1.33	EIF386	8q22-q23	murine mammary tumor integration site 6 (oncogene homolog)	eukaryotic translation initiation factor 3, subunit 6 (48kD)
RSU1	L12535_at	PASS		9	13.44	PASS	13	9	10.08	1.33	1.33	RSU-1		homologous to mouse Rsu-1; putative	homologous to mouse Rsu-1; putative

SFRS7_ma1	L41887_ma1	L41887	PASS	6	6.33	PASS	8	6	4.75	1.33	1.33	SFRS7	splicing factor, arginine/serine-rich 7	35 kDa protein
K71	D31888_at	D31888	PASS	8	7.25	PASS	9	8	5.44	1.33	1.33	KIAA0071		
ANT3	J03592_at	J03592	PASS	9	200.78	PASS	13	9	151.00	1.33	1.33	ANT3		adenine nucleotide translocator 3 (liver)
MDH1	D55654_at	D55654	PASS	9	25.36	PASS	13	9	19.23	1.33	1.33	KPNB4		karyopherin alpha 4 (importin alpha 3)
RPLP2	AB002533_at	AB002533	PASS	9	355.11	PASS	13	9	267.23	1.33	1.33	PSMB1		proteasome (prosome, macropain) subunit, beta type, 1
PSMA5	D00761_at	D00761	PASS	9	33.11	PASS	13	9	24.92	1.33	1.33	NPM1		nucleophosmin (nucleolar phosphoprotein B23, numatrin)
NPM1	M23613_at	M23613	PASS	9	103.33	PASS	13	9	77.85	1.33	1.33	KIAA0002		KIAA0002 gene product
K2_TRIC5	D13627_at	D13627	PASS	9	15.78	PASS	12	9	11.92	1.32	1.32	GZMK		granzyme K (serine protease, granzyme 3; tryptase II)
GZMK	U26174_at	U26174	PASS	6	17.50	PASS	13	6	13.23	1.32	1.32	CD2		CD2 antigen (p50), sheep red blood cell receptor
MRP	X78338_at	X78338	PASS	7	7.43	PASS	8	7	5.63	1.32	1.32	KIAA0164		KIAA0164 gene product
M16336_s_at	M16336_s_at	M16336	PASS	9	52.11	PASS	13	9	39.54	1.32	1.32	RPL17		ribosomal protein L17
K164_DNAB	D79986_at	D79986	PASS	8	16.63	PASS	13	8	12.62	1.32	1.32	SPHAR		steroid receptor coactivator 1
RPL17	X53777_at	X53777	PASS	9	206.44	PASS	13	9	156.69	1.32	1.32	FLI1		Friend leukemia virus integration 1
SPHAR	X82554_ma1	X82554	PASS	5	6.00	PASS	9	5	4.56	1.32	1.32	KIAA0016		KIAA0016 gene product
SRC1	U59302_at	U59302	PASS	9	11.44	PASS	13	9	8.69	1.32	1.32	CLAPS3		clathrin-associated/assembly/adaptor protein, small 3 (22kD)
FLI1	M98833_at	M98833	PASS	7	8.29	PASS	13	7	6.31	1.31	1.31	RPS28		ribosomal protein S28
K16	D13641_at	D13641	PASS	8	13.13	PASS	13	8	10.00	1.31	1.31	rab11a		GTPase
TFAP3S	U91932_at	U91932	PASS	9	14.33	PASS	13	9	10.92	1.31	1.31	HPRT1		hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)
GUASMPST	HG4716-HT3	HG4716-H	PASS	8	7.75	PASS	11	8	5.91	1.31	1.31	PSMD1		proteasome (prosome, macropain) 26S subunit, non-ATPase, 1
RPS28	U58682_at	U58682	PASS	9	286.67	PASS	13	9	218.69	1.31	1.31	CBFA3		core-binding factor, runt domain, alpha subunit 3
RAB11A	AF000231_at	AF000231	PASS	6	6.17	PASS	7	6	4.71	1.31	1.31	PSMD8		proteasome (prosome, macropain) 26S subunit, non-ATPase, 8
AFFX-HUM4	AFFX-HUM4	AFFX-HUM4	PASS	6	12.17	PASS	13	6	9.31	1.31	1.31	PSMC6		proteasome (prosome, macropain) 26S subunit, ATPase, 6
HPRT1	M31642_at	M31642	PASS	8	7.63	PASS	12	8	5.83	1.31	1.31	76 kDa membrane protein		76 kDa membrane protein
PSM112	D44466_at	D44466	PASS	9	7.44	PASS	10	9	5.70	1.31	1.31	KIAA0054		KIAA0054 gene product
PEBP2AC1	Z35278_at	Z35278	PASS	9	19.78	PASS	13	9	15.15	1.31	1.31	nuclear protein Skip		nuclear protein Skip
PSMCP31	D38047_at	D38047	PASS	9	31.22	PASS	13	9	23.92	1.31	1.31			
PSM42	D78275_at	D78275	PASS	8	9.25	PASS	10	8	7.10	1.30	1.30			
P76	U81006_at	U81006	PASS	7	9.00	PASS	11	7	6.91	1.30	1.30			
K54_MOV10	D29677_at	D29677	PASS	7	8.29	PASS	11	7	6.36	1.30	1.30			
SKIP	U51432_at	U51432	PASS	6	13.00	PASS	10	6	10.00	1.30	1.30			

K256	D87445_at	D87445	PASS	6	6.50	PASS	9	6	5.00	1.30	1.30	KIAA0256			KIAA0256 gene product
LGALS8	L78132_at	L78132	PASS	6	6.17	PASS	8	6	4.75	1.30	1.30	pcta-1			prostate carcinoma tumor antigen
POLR2	U37689_at	U37689	PASS	5	9.80	PASS	9	5	7.56	1.30	1.30	hsRPE8			RNA polymerase II subunit
CASP10	U60519_at	U60519	PASS	6	6.67	PASS	7	6	5.14	1.30	1.30	CASP10	2q33-q34		caspase 10, apoptosis-related cysteine protease
LI4778_s_at	LI4778_s_at	LI4778	PASS	9	9.78	PASS	11	9	7.55	1.30	1.30	PPP3CA	4q21-q24		calmodulin-dependent phosphatase catalytic subunit
RAB_ma1	I42025_ma1	I42025	PASS	6	6.33	PASS	9	6	4.89	1.30	1.30	HRB	2q36		HIV-1 Rev binding protein
GAPDHM	AFFX-HUMAFHX-HUN	AFFX-HUMAFHX-HUN	PASS	9	162.00	PASS	13	9	125.31	1.29	1.29				
IE_121711DM	U92014_at	U92014	PASS	6	6.83	PASS	7	6	5.29	1.29	1.29				
HRMT1L1	X99209_at	X99209	PASS	9	20.78	PASS	13	9	16.08	1.29	1.29				arginine methyltransferase
RPL10	HG4542-HT4HG4542-H	HG4542-HT4HG4542-H	PASS	9	184.78	PASS	13	9	143.08	1.29	1.29				
28SRNA5	AFFX-M278	AFFX-M278	PASS	7	8.71	PASS	8	7	6.75	1.29	1.29				
YWHA	X56468_at	X56468	PASS	9	23.33	PASS	13	9	18.08	1.29	1.29				
ACADM	M91432_at	M91432	PASS	8	7.50	PASS	11	8	5.82	1.29	1.29	ACADM	1p31		acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain
FMR1	U25165_at	U25165	PASS	7	11.00	PASS	13	7	8.54	1.29	1.29	FXR1	3q28		fragile X mental retardation, autosomal homolog 1
HMG17_ma	X13546_ma1	X13546	PASS	9	40.22	PASS	13	9	31.23	1.29	1.29	HMG17	1p36.1-p35		high-mobility group (nonhistone chromosomal) protein 17
K6_VAV1	D25304_at	D25304	PASS	9	16.11	PASS	13	9	12.54	1.28	1.28	KIAA0006			PAK-interacting exchange factor alpha
SNRPD2	U15008_at	U15008	PASS	9	140.33	PASS	13	9	109.23	1.28	1.28	SNRPD2			small nuclear ribonucleoprotein D2
COX5A	M22760_at	M22760	PASS	9	16.89	PASS	13	9	13.15	1.28	1.28	COX5A	15q25		polypeptide (16.5kD) cytochrome c oxidase subunit Va
VRK1	AB000449_a	AB000449	PASS	7	7.57	PASS	10	7	5.90	1.28	1.28	VRK1	14q32		vaccinia related kinase 1
M31516_s_a	M31516_s_a	M31516	PASS	5	6.20	PASS	12	5	4.83	1.28	1.28	DAF	1q32		decay accelerating factor for complement (CD55, Crmer blood group system)
TRPSL	M23161_at	M23161	PASS	7	6.29	PASS	11	7	4.91	1.28	1.28				
PSMC5	L38810_at	L38810	PASS	9	14.67	PASS	11	9	11.45	1.28	1.28	PSMC5	17q23-q25		proteasome (prosome, macropain) 26S subunit, ATPase, 5
UROD	M14016_at	M14016	PASS	7	7.86	PASS	7	7	6.14	1.28	1.28	UROD	1p34		uroporphyrinogen decarboxylase
POLR2	HG2274-HT3HG2274-H	HG2274-HT3HG2274-H	PASS	6	10.33	PASS	12	6	8.08	1.28	1.28				
M96954_s_a	M96954_s_a	M96954	PASS	9	7.67	PASS	13	9	6.00	1.28	1.28				nucleolysin TIAR
TRP185	U38847_at	U38847	PASS	5	6.20	PASS	7	5	4.86	1.28	1.28	TRP-185			TAR RNA loop binding protein
GCNT1	U77413_at	U77413	PASS	5	7.40	PASS	10	5	5.80	1.28	1.28	OGT			O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-beta-N-acetylglucosaminyl transferase)
RAN	HG1112-HT	HG1112-H	PASS	9	21.44	PASS	13	9	16.85	1.27	1.27				inducible poly(A)-binding protein
INDPOLABH	U33818_at	U33818	PASS	8	14.88	PASS	13	8	11.69	1.27	1.27	IPABP			dolichyl-phosphate mannosyltransferase
DPM1	AF007875_at	AF007875	PASS	8	8.38	PASS	12	8	6.58	1.27	1.27	DPM1			dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit

TCF3	M31523_at	M31523	PASS	9	6.89	PASS	12	9	5.42	1.27	1.27	1.27	19		transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)
Z26491_s at	Z26491_s at	Z26491	PASS	9	13.89	PASS	13	9	10.92	1.27	1.27	1.27		catechol O-methyltransferase	
HNRNPCL	M94630_at	M94630	PASS	9	27.56	PASS	13	9	21.69	1.27	1.27	1.27	4q21	heterogeneous nuclear ribonucleoprotein D	heterogeneous nuclear ribonucleoprotein D
K212_COSC	D86967_at	D86967	PASS	7	11.43	PASS	12	7	9.00	1.27	1.27	1.27		KIAA0212 gene product	KIAA0212 gene product
EIF2A	U26032_at	U26032	PASS	5	5.80	PASS	7	5	4.57	1.27	1.27	1.27	3p22	transforming growth factor, beta receptor II (70-80kD)	transforming growth factor, beta receptor II (70-80kD)
TCFBR2	D50683_at	D50683	PASS	9	24.00	PASS	13	9	18.92	1.27	1.27	1.27		protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform
PPP2R2A	M64929_at	M64929	PASS	7	7.29	PASS	8	7	5.75	1.27	1.27	1.27		G protein-coupled receptor kinase 5	G protein-coupled receptor kinase 5
GPRK5	L15388_at	L15388	PASS	6	6.33	PASS	7	6	5.00	1.27	1.27	1.27	10q24-qter	calcineurin A2	calcineurin A2
PPP3CB2	M29551_at	M29551	PASS	5	7.60	PASS	9	5	6.00	1.27	1.27	1.27		cyclin H	cyclin H
HG3484-HT3	HG3484-HT3	HG3484-H	PASS	7	8.86	PASS	12	7	7.00	1.27	1.27	1.27	5q13.3-q14	H2A histone family, member Q	H2A histone family, member Q
CCNH	U11791_at	U11791	PASS	7	6.43	PASS	12	7	5.08	1.26	1.26	1.26	1q21-q23	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)
H2B_ma2	X57985_ma2	X57985	PASS	9	9.11	PASS	13	9	7.23	1.26	1.26	1.26	4q24	thyroid autoantigen 70kD (Ku antigen)	thyroid autoantigen 70kD (Ku antigen)
NFKB1	M58603_at	M58603	PASS	6	16.17	PASS	12	6	12.83	1.26	1.26	1.26		Rab geranylgeranyltransferase, beta subunit	Rab geranylgeranyltransferase, beta subunit
G22P1	J04611_at	J04611	PASS	9	23.44	PASS	13	9	18.62	1.26	1.26	1.26	22q11-q13	enoyl Coenzyme A hydratase 1, peroxisomal	enoyl Coenzyme A hydratase 1, peroxisomal
RABGGTB	X98001_at	X98001	PASS	6	6.67	PASS	10	6	5.30	1.26	1.26	1.26	1p31-p22	Similar to Scerevisiae hypothetical protein L3111 (S59316)	Similar to Scerevisiae hypothetical protein L3111 (S59316)
ECH1	U16660_at	U16660	PASS	7	20.57	PASS	13	7	16.38	1.26	1.26	1.26	19q13.1	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1
K276_HYPL	D87466_at	D87466	PASS	7	5.71	PASS	9	7	4.56	1.25	1.25	1.25		catechol-O-methyltransferase	catechol-O-methyltransferase
K78_RAD21	D38551_at	D38551	PASS	8	10.63	PASS	12	8	8.50	1.25	1.25	1.25		zinc finger protein 43 (HITF6)	zinc finger protein 43 (HITF6)
ECGF1	M31210_at	M31210	PASS	8	6.38	PASS	10	8	5.10	1.25	1.25	1.25	1pter-qter	macrophage migration inhibitory factor (glycosylation-inhibiting factor)	macrophage migration inhibitory factor (glycosylation-inhibiting factor)
M58325_s at	M58525_s at	M58525	PASS	5	10.40	PASS	12	5	8.33	1.25	1.25	1.25	22q11.21-q11.23	interleukin 16 (lymphocyte chemoattractant factor)	interleukin 16 (lymphocyte chemoattractant factor)
HG2639-HT2	HG2639-HT2	HG2639-H	PASS	9	11.89	PASS	13	9	9.54	1.25	1.25	1.25		cathepsin S	cathepsin S
ZNF43_f	X59244_f at	X59244	PASS	5	5.60	PASS	10	5	4.50	1.24	1.24	1.24		enhancer of rudimentary (Drosophila) homolog	enhancer of rudimentary (Drosophila) homolog
D79984_s at	D79984_s at	D79984	PASS	5	6.40	PASS	7	5	5.14	1.24	1.24	1.24			
MIF_ma1	L19686_ma1	L19686	PASS	9	43.33	PASS	13	9	34.85	1.24	1.24	1.24	22q11.2		
CBF	M37197_at	M37197	PASS	8	6.75	PASS	7	8	5.43	1.24	1.24	1.24			
M90391_s at	M90391_s at	M90391	PASS	7	7.71	PASS	9	7	6.22	1.24	1.24	1.24			
K29	D21852_at	D21852	PASS	9	7.33	PASS	12	9	5.92	1.24	1.24	1.24			
CTSS	M90696_at	M90696	PASS	8	12.38	PASS	11	8	10.00	1.24	1.24	1.24	1q21		
X15673_s at	X15673_s at	X15673	PASS	5	9.40	PASS	10	5	7.60	1.24	1.24	1.24			
ERH	D85758_at	D85758	PASS	7	21.86	PASS	13	7	17.69	1.24	1.24	1.24	7q34		

HUM431	U30521_at	U30521	PASS	5	6.00	PASS	7	5	4.86	1.24	1.24	1.23	1.23	P311	P311 protein	P311 protein similar to human transcription factor TFIIIS (S34159).
K244_TCEA	D87685_at	D87685	PASS	8	5.63	PASS	9	8	4.56	1.23	1.23	1.23	1.23	KIAA0244		
PSM1131	D88378_at	D88378	PASS	6	6.00	PASS	8	6	4.88	1.23	1.23	1.23	1.23		proteasome inhibitor hP131 subunit	
SRI	M32886_at	M32886	PASS	8	7.00	PASS	13	8	5.69	1.23	1.23	1.23	1.23	SRI	srcin	srcin
PRKARIA	M33336_at	M33336	PASS	7	25.71	PASS	13	7	20.92	1.23	1.23	1.23	1.23	PRKARIA	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extingisher 1)	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extingisher 1)
AMD1	M21154_at	M21154	PASS	8	8.50	PASS	12	8	6.92	1.23	1.23	1.23	1.23	AMD1	S-adenosylmethionine decarboxylase 1	S-adenosylmethionine decarboxylase 1
HG884-HT8	HG884-HT8	HG884-HT8	PASS	5	6.00	PASS	9	5	4.89	1.23	1.23	1.23	1.23			This sequence comes from Fig. 4.
RAB5IP	S83364_at	S83364	PASS	7	11.86	PASS	12	7	9.67	1.23	1.23	1.23	1.23			
K35_NOP1	D21262_at	D21262	PASS	9	7.11	PASS	10	9	5.80	1.23	1.23	1.23	1.23	P130	nucleolar phosphoprotein p130	nucleolar phosphoprotein p130
CD36	Z32765_at	Z32765	PASS	8	26.88	PASS	13	8	21.92	1.23	1.23	1.23	1.23			
ETFA	J04058_at	J04058	PASS	7	6.57	PASS	11	7	5.36	1.23	1.23	1.23	1.23	ETFA	electron-transfer-flavoprotein, alpha polypeptide (glutaric aciduria II)	electron-transfer-flavoprotein, alpha polypeptide (glutaric aciduria II)
TCEA1	M81601_at	M81601	PASS	8	18.75	PASS	13	8	15.31	1.22	1.22	1.22	1.22	transcriptio n elongation actin	transcription elongation factor SII	
GSN	S65738_at	S65738	PASS	9	10.00	PASS	12	9	8.17	1.22	1.22	1.22	1.22		actin depolymerizing factor	This sequence comes from Fig. 1B, destrin; ADF
D78132_s_at	D78132_s_at	D78132	PASS	8	7.63	PASS	13	8	6.23	1.22	1.22	1.22	1.22	Rheb	ras-related GTP-binding protein	Ras homologue enriched in brain; similar to rat Rheb gene
ITPR2	D26070_at	D26070	PASS	5	5.80	PASS	12	5	4.75	1.22	1.22	1.22	1.22	ITPR1	human type 1 inositol 1,4,5-trisphosphate receptor	inositol 1,4,5-trisphosphate receptor, type 1
HG210-HT2	HG210-HT2	HG210-HT2	PASS	5	5.80	PASS	8	5	4.75	1.22	1.22	1.22	1.22			
U28488_s_at	U28488_s_at	U28488	PASS	5	7.20	PASS	10	5	5.90	1.22	1.22	1.22	1.22	C3AR1	complement component 3a receptor 1	complement component 3a receptor 1
EGR1	S81439_at	S81439	PASS	7	5.86	PASS	10	7	4.80	1.22	1.22	1.22	1.22	TIEG	TGFβ inducible early growth response	TGFβ inducible early growth response
TSC22	U35048_at	U35048	PASS	9	15.11	PASS	13	9	12.38	1.22	1.22	1.22	1.22	TSC22	TSC-22 protein	transforming growth factor beta-stimulated protein TSC-22
DCN	M14219_at	M14219	PASS	7	7.43	PASS	11	7	6.09	1.22	1.22	1.22	1.22	DCN	decorin	decorin
U00947_s_at	U00947_s_at	U00947	PASS	9	88.89	PASS	13	9	72.92	1.22	1.22	1.22	1.22			
K155_COSB	D63875_at	D63875	PASS	8	7.88	PASS	13	8	6.46	1.22	1.22	1.22	1.22	KIAA0155	KIAA0155 gene product	KIAA0155 gene product
X57152_mal	X57152_mal	X57152	PASS	9	28.00	PASS	13	9	23.00	1.22	1.22	1.22	1.22		casein kinase II subunit beta	protein kinase
Y00451_s_at	Y00451_s_at	Y00451	PASS	8	5.75	PASS	11	8	4.73	1.22	1.22	1.22	1.22	ALAS2	aminolevulinate, delta-, synthase 2 (sideroblastic/hypochromic anemia)	aminolevulinate, delta-, synthase 2 (sideroblastic/hypochromic anemia)





ERP31	X94910_at	X94910	PASS	8	19.25	PASS	13	8	16.46	1.17	1.17	ERp28	Similar to ULA_5 product, AC P30040
TCP1	X52882_at	X52882	PASS	8	11.38	PASS	12	8	9.75	1.17	1.17		t-complex polypeptide 1 (AA 1-556)
DAP5	AFX-DapX-AFFX-Dap		PASS	9	242.44	PASS	13	9	207.85	1.17	1.17		
SGTPBP	U57094_at	U57094	PASS	6	11.00	PASS	9	6	9.44	1.16	1.16	RAB27A	RAB27A, member RAS oncogene family
SF2P32	M69039_at	M69039	PASS	8	9.13	PASS	13	8	7.85	1.16	1.16	C1QBP	complement component 1, q subcomponent binding protein
UBE2A	M74524_at	M74524	PASS	7	6.00	PASS	12	7	5.17	1.16	1.16	UBE2A	ubiquitin-conjugating enzyme E2A (RAD6 homolog)
CCT4	U38846_at	U38846	PASS	9	30.67	PASS	13	9	26.46	1.16	1.16	SRB	stimulator of TAR RNA binding
FRG1	L76159_at	L76159	PASS	6	7.67	PASS	13	6	6.62	1.16	1.16	FRG1	FSHD region gene 1
M57466_s_at	M57466_s_at	M57466	PASS	9	70.67	PASS	13	9	61.08	1.16	1.16	HLA-DPB1	major histocompatibility complex, class II, DP beta 1
U44799_s_at	U44799_s_at	U44799	PASS	6	6.00	PASS	10	6	5.20	1.15	1.15		U1-snRNP binding protein homolog
RASA1	M23379_at	M23379	PASS	5	6.00	PASS	10	5	5.20	1.15	1.15	RASA1	RAS p21 protein activator (GTPase activating protein) 1
J02621_s_at	J02621_s_at	J02621	PASS	9	26.44	PASS	13	9	22.92	1.15	1.15	HMG14	21q22.3
YES1	M15990_at	M15990	PASS	7	5.43	PASS	7	7	4.71	1.15	1.15	YES1	18p11.31-pl1.21
CTSL	X12451_at	X12451	PASS	6	6.33	PASS	10	6	5.50	1.15	1.15	CTSL	9q21-q22
W19119	M24069_at	M24069	PASS	7	6.71	PASS	12	7	5.83	1.15	1.15	CSDA	12p13.1
Z25521_s_at	Z25521_s_at	Z25521	PASS	9	16.11	PASS	13	9	14.00	1.15	1.15		integrin associated protein
CISACTS	M82882_at	M82882	PASS	7	7.86	PASS	12	7	6.83	1.15	1.15	ELF1	
K181	D80003_at	D80003	PASS	8	6.13	PASS	12	8	5.33	1.15	1.15	KIAA0181	
CAMLG	U18242_at	U18242	PASS	7	6.57	PASS	11	7	5.73	1.15	1.15	CAMLG	5q23
RANBP1	D38076_at	D38076	PASS	7	9.00	PASS	13	7	7.85	1.15	1.15	RANBP1	RAN binding protein 1
ICT1	X81788_at	X81788	PASS	7	6.14	PASS	11	7	5.36	1.15	1.15	ICT1	immature colon carcinoma transcript 1
RB1	L41870_at	L41870	PASS	7	5.86	PASS	8	7	5.13	1.14	1.14	RB1	13q14.2
K254	D87443_at	D87443	PASS	7	4.57	PASS	7	7	4.00	1.14	1.14	KIAA0254	
HG1428-HT	HG1428-HT	HG1428-HT	PASS	9	286.67	PASS	13	9	250.92	1.14	1.14		calcium modulating ligand
M31520_ma	M31520_ma	M31520	PASS	9	154.78	PASS	13	9	135.54	1.14	1.14	tps24	RAN binding protein 1
NAPIL1	M86667_at	M86667	PASS	9	33.78	PASS	13	9	29.62	1.14	1.14	NAPIL1	immature colon carcinoma transcript 1
RBM3	U28686_at	U28686	PASS	8	12.13	PASS	11	8	10.64	1.14	1.14	RBM3	13q14.2
U58046_s_at	U58046_s_at	U58046	PASS	5	5.80	PASS	10	5	5.10	1.14	1.14	EIF3S10	retinoblastoma 1 (including osteosarcoma)
VBP1	U56833_at	U56833	PASS	8	6.38	PASS	13	8	5.62	1.14	1.14	VBP1	von Hippel-Lindau binding protein 1
TCLLYM_ma	X82240_ma	X82240	PASS	5	15.20	PASS	12	5	13.42	1.13	1.13	TCL1A	von Hippel-Lindau binding protein 1
ACP1	U25849_at	U25849	PASS	6	9.83	PASS	13	6	8.69	1.13	1.13	ACP1	T cell leukemia/lymphoma 1
M60483_ma	M60483_ma	M60483	PASS	8	6.50	PASS	12	8	5.75	1.13	1.13	PPP2CA	acid phosphatase 1, soluble



PSMHC8	D00762_at	D00762	PASS	7	11.43	PASS	9	7	10.11	1.13	1.13	PSMA3	14q23	proteasome (prosome, macropain) subunit, alpha type, 3	proteasome (prosome, macropain) subunit, alpha type, 3
LGALS2	M87860_at	M87860	PASS	7	26.71	PASS	11	7	23.64	1.13	1.13	LGALS2	1q32.1	S-lac lectin	proteasome (prosome, macropain) subunit, alpha type, 3
D11327_s_at	D11327_s_at	D11327	PASS	8	5.75	PASS	10	8	5.10	1.13	1.13	PTPN7	1q32.1	protein tyrosine phosphatase, non-receptor type 7	protein tyrosine phosphatase, non-receptor type 7
BFS3	L34587_at	L34587	PASS	9	13.78	PASS	13	9	12.23	1.13	1.13			RNA polymerase II elongation factor III, p15 subunit	putative
FEZ2	U60061_at	U60061	PASS	6	5.83	PASS	11	6	5.18	1.13	1.13	FEZ2		myocyte-specific enhancer factor 2A, C4 form	zygote 2
U49020_cds3	U49020_cds3	U49020	PASS	8	5.75	PASS	9	8	5.11	1.13	1.13	MEF2A		protein phosphatase 1B (formerly 2C), magnesium-dependent, beta isoform	protein phosphatase 1B (formerly 2C), magnesium-dependent, beta isoform
PPM1A	S87759_at	S87759	PASS	7	6.00	PASS	9	7	5.33	1.13	1.13	PPM1B		eukaryotic translation initiation factor 4A, isoform 2	eukaryotic translation initiation factor 4A, isoform 2
EIF4A2	D30655_at	D30655	PASS	9	60.56	PASS	13	9	53.85	1.12	1.12	EIF4A2	18p11.2	thiopyrimine methyltransferase	35 kDa monomer; cytosolic protein
GRUB	HG4582-HT4	HG4582-HT4	PASS	5	5.60	PASS	11	5	5.00	1.12	1.12	TPMT		C-Type lectin	C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 2 (activation-induced)
U12387_s_at	U12387_s_at	U12387	PASS	5	6.60	PASS	10	5	5.90	1.12	1.12			proteasome (prosome, macropain) subunit, alpha type, 5	proteasome (prosome, macropain) subunit, alpha type, 5
AICL	X96719_at	X96719	PASS	5	18.40	PASS	13	5	16.46	1.12	1.12	CLECSF2	12p	phosphoribosyl pyrophosphate synthetase 1	phosphoribosyl pyrophosphate synthetase 1
K69_DS0556	D31885_at	D31885	PASS	9	16.56	PASS	13	9	14.85	1.12	1.12	KIAA0069		adenosine kinase	adenosine kinase
PSMA5	X61970_at	X61970	PASS	9	13.11	PASS	13	9	11.77	1.11	1.11	PSMA5	1p13	SLP-76	76 kDa tyrosine phosphoprotein
PRPS1	D00860_at	D00860	PASS	9	6.11	PASS	12	9	5.50	1.11	1.11	PRPS1	Xq21-q27	peptidylprolyl isomerase B (cyclophilin B)	peptidylprolyl isomerase B (cyclophilin B)
U33936_s_at	U33936_s_at	U33936	PASS	7	5.86	PASS	11	7	5.27	1.11	1.11	ADK	10cen-q24	protein phosphatase B56-epsilon	protein phosphatase 2, regulatory subunit B (B56), epsilon isoform
LCP2	U20158_at	U20158	PASS	9	17.00	PASS	13	9	15.31	1.11	1.11				
HG2981-HT3	HG2981-HT3	HG2981-HT3	PASS	7	10.29	PASS	11	7	9.27	1.11	1.11				
PP1B	M63573_at	M63573	PASS	7	17.29	PASS	12	7	15.58	1.11	1.11	PP1B	15		
B56E	L76703_at	L76703	PASS	6	5.17	PASS	9	6	4.67	1.11	1.11	PPP2R5E	7p11.2-p12		
E_23801	U79282_at	U79282	PASS	5	5.20	PASS	10	5	4.70	1.11	1.11				
HSPA8	HG2855-HT4	HG2855-HT4	PASS	9	38.56	PASS	13	9	35.00	1.10	1.10				
H2AZ	M37583_at	M37583	PASS	9	18.11	PASS	13	9	16.46	1.10	1.10	H2AFZ	4q24	H2A histone family, member Z	H2A histone family, member Z
PHC11	J04973_at	J04973	PASS	9	12.78	PASS	13	9	11.62	1.10	1.10	UQCRC2	16p12	ubiquinol-cytochrome c reductase core protein II	ubiquinol-cytochrome c reductase core protein II
TCRD	M21624_at	M21624	PASS	9	17.33	PASS	13	9	15.77	1.10	1.10	TCRD	14q11.2	T-cell receptor, delta (V.D.J.C)	T-cell receptor, delta (V.D.J.C)
TNFAIP3	M59465_at	M59465	PASS	9	13.33	PASS	13	9	12.15	1.10	1.10	TNFAIP1	17q22-q23	tumor necrosis factor, alpha-induced protein 1 (endothelial)	tumor necrosis factor, alpha-induced protein 1 (endothelial)
APBB1	U50939_at	U50939	PASS	7	6.57	PASS	12	7	6.00	1.10	1.10	APPBP1	16q22	Amyloid beta precursor protein-binding protein 1	Amyloid beta precursor protein-binding protein 1, 59kD
BACTINM	AFFX-HSAC	AFFX-HSAC	PASS	9	330.67	PASS	13	9	302.92	1.09	1.09				
D13824E	U47635_at	U47635	PASS	6	6.67	PASS	9	6	6.11	1.09	1.09				
RAD23B	D21090_at	D21090	PASS	7	6.00	PASS	12	7	5.50	1.09	1.09	RAD23B	3p25.1	DSEF number: D13824E; orf	DSEF number: D13824E; orf
															RAD23 (S. cerevisiae) homolog B

PSMD4	U24704_at	U24704	PASS	7	11.29	PASS	11	7	10.36	1.09	1.09	antisecretory factor-1	similar to Human S5a proteasome subunit, Genbank Accession Number U51007
PRKMK1	L11284_at	L11284	PASS	7	10.29	PASS	13	7	9.46	1.09	1.09	15q22.1-q22.33	protein kinase, mitogen-activated, kinase 1 (MAP kinase kinase 1)
BI0B5	AFFX-BioB-AFFX-BioB	L13848	PASS	9	113.56	PASS	13	9	104.69	1.08	1.08	1q25	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 9 (RNA helicase A, nuclear DNA helicase II; leukophycin)
LKP	L13848_at	L13848	PASS	6	10.83	PASS	10	6	10.00	1.08	1.08		DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 9 (RNA helicase A, nuclear DNA helicase II; leukophycin)
EFTS	L37936_at	L37936	PASS	8	10.38	PASS	12	8	9.58	1.08	1.08		elongation factor Ts
CBX	U35451_at	U35451	PASS	6	6.17	PASS	10	6	5.70	1.08	1.08	p25beta	heterochromatin protein p25
SMN1_ma3	U80017_ma3	U80017	PASS	7	6.00	PASS	9	7	5.56	1.08	1.08	btf2p44	basic transcription factor 2 p44
X03689_s_at	X03689_s_at	X03689	PASS	9	224.56	PASS	13	9	208.08	1.08	1.08	20q13.3	eukaryotic translation factor 1 alpha 2
PRPS2	Y00971_at	Y00971	PASS	5	5.00	PASS	11	5	4.64	1.08	1.08	Xpter-q21	eukaryotic translation factor 1 alpha 2
ATP5C1	D16562_at	D16562	PASS	9	29.67	PASS	13	9	27.54	1.08	1.08		phosphoribosyl pyrophosphate synthetase 2
K191	D83776_at	D83776	PASS	5	6.00	PASS	7	5	5.57	1.08	1.08	KIAA0191	ATP synthase gamma-subunit
M67468_s_at	M67468_s_at	M67468	PASS	7	5.14	PASS	9	7	4.78	1.08	1.08		The KIAA0191 gene is expressed ubiquitously; The KIAA0191 protein retains the C2H2 zinc-finger at its N-terminal region.
ANX7	J04543_at	J04543	PASS	8	8.25	PASS	12	8	7.67	1.08	1.08	Xq27.3	fragile X mental retardation 1
CMKBR7	L08177_at	L08177	PASS	8	5.38	PASS	10	8	5.00	1.08	1.08	10q21.1-q21.2	anxin VII (synexin)
NIFUL	U47101_at	U47101	PASS	9	26.78	PASS	13	9	24.92	1.07	1.07	EBI2	Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-coupled receptor)
K242_HYP5	D87684_at	D87684	PASS	8	8.13	PASS	10	8	7.60	1.07	1.07	EBI2	Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-coupled receptor)
LCP1	J02923_at	J02923	PASS	9	45.67	PASS	13	9	42.77	1.07	1.07	13q14.3	Similar to N-terminal regions of diazotroph NifU proteins
S203_15	L40395_at	L40395	PASS	8	6.50	PASS	9	8	6.11	1.06	1.06		Similar to a C.elegans ZK353.8 protein (S44655)
LAML	HG1078-HT	HG1078-HT	PASS	7	13.00	PASS	13	7	12.23	1.06	1.06		lymphocyte cytosolic protein 1 (L-plastin)
PBX3	X59841_at	X59841	PASS	6	5.67	PASS	9	6	5.33	1.06	1.06	9q33-q34	ORF; putative
SRP9	U20998_at	U20998	PASS	9	15.44	PASS	13	9	14.54	1.06	1.06		pre-B-cell leukemia transcription factor 3
L33930_s_at	L33930_s_at	L33930	PASS	6	4.67	PASS	10	6	4.40	1.06	1.06		signal recognition particle 9kD
CGR19	U66469_at	U66469	PASS	5	5.40	PASS	10	5	5.10	1.06	1.06		signal transducer CD24
SRPK2	U88666_at	U88666	PASS	8	5.38	PASS	12	8	5.08	1.06	1.06	7q22-q31.1	cell growth regulator CGR19
B2M	S82297_at	S82297	PASS	9	164.00	PASS	13	9	155.15	1.06	1.06	15q21-q22.2	SFRS protein kinase 2
SRP54	U51920_at	U51920	PASS	6	5.17	PASS	10	6	4.90	1.05	1.05		beta-2-microglobulin
U84011_s_at	U84011_s_at	U84011	PASS	5	4.80	PASS	9	5	4.56	1.05	1.05	1p21	beta-2-microglobulin
E_23865	U90912_at	U90912	PASS	7	5.71	PASS	7	7	5.43	1.05	1.05		signal recognition particle 54kD
SFRS3	U30825_at	U30825	PASS	9	31.44	PASS	13	9	29.92	1.05	1.05		anylo-1,6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III)
													splicing factor, arginine/serine-rich 9

HNRP12	U01923	PASS	7	6.71	PASS	10	7	6.40	1.05	1.05	RPL14	ribosomal protein L14
RPL14	D87735	PASS	9	150.33	PASS	13	9	143.31	1.05	1.05		
W52B f	HG3576-HT3HG3576-H	PASS	9	106.89	PASS	13	9	102.08	1.05	1.05		
AMFR	M63175	PASS	5	6.80	PASS	8	5	6.50	1.05	1.05	AMFR	autocrine motility factor receptor
K73_CYCRP	D38552	PASS	6	6.83	PASS	13	6	6.54	1.05	1.05	KIAA0073	The ha1539 protein is related to cyclophilin
MCM3	D38073	PASS	8	6.88	PASS	10	8	6.60	1.04	1.04	MCM3	minichromosome maintenance deficient (S. cerevisiae) 3
PAK3	U25975	PASS	5	5.60	PASS	10	5	5.40	1.04	1.04	hPAK65	rac/CDC42Hs activated kinase; serine kinase; Method: conceptual translation supplied by author
U67122_s at	U67122_s at	PASS	7	11.00	PASS	13	7	10.62	1.04	1.04	SUMO-1	conjugated post-translationally to RanGAP1; ubiquitin-related protein; similar to UBL1 encoded by GenBank Accession Number U38784, PIC1 encoded by GenBank Accession Number U61397 and GMP1 encoded by GenBank Accession Number U72722
L06797_s at	L06797_s at	PASS	9	33.67	PASS	13	9	32.54	1.03	1.03	CXCR4	chemokine (C-X-C motif), receptor 4 (fusin)
CAT_ma1	X04085	PASS	7	15.43	PASS	13	7	14.92	1.03	1.03		catalase
SFRS3	D28423	PASS	6	17.33	PASS	12	6	16.83	1.03	1.03		pre-mRNA splicing factor
J02683_s at	J02683_s at	PASS	9	31.56	PASS	13	9	30.69	1.03	1.03	ANT2	adenine nucleotide translocator 2 (fibroblast)
RPS7_ma1	Z25749	PASS	9	136.56	PASS	13	9	132.85	1.03	1.03	RPS7	ribosomal protein S7
HDAC2	U31814	PASS	9	6.78	PASS	10	9	6.60	1.03	1.03	HDAC2	histone deacetylase 2
M60974_s at	M60974_s at	PASS	5	5.60	PASS	10	5	5.50	1.02	1.02	DDIT1	DNA-damage-inducible transcript 1
SEMA	U60800	PASS	9	22.22	PASS	13	9	21.85	1.02	1.02	CD100	semaphorin
D13631_s at	D13631_s at	PASS	7	11.00	PASS	12	7	10.83	1.02	1.02	KIAA0006	
PRKACB	M34181	PASS	5	6.80	PASS	10	5	6.70	1.01	1.01	PRKACB	protein kinase, cAMP-dependent, catalytic, beta
M26730_s at	M26730_s at	PASS	9	33.78	PASS	13	9	33.31	1.01	1.01	UQBP	ubiquitin-binding protein (QP)
GDI2	D13988	PASS	6	18.17	PASS	13	6	18.00	1.01	1.01	GDI2	GDP dissociation inhibitor 2
RPL44	M15661	PASS	9	51.44	PASS	13	9	51.08	1.01	1.01	RPL44	ribosomal protein L44
ZFPRES24_2	AB000468	PASS	8	18.75	PASS	13	8	18.69	1.00	1.00	RNF4	ring finger protein 4
BACTIN5	AFFX-HSAC	PASS	9	240.44	PASS	13	9	240.00	1.00	1.00		
M87507_s at	M87507_s at	PASS	6	7.50	PASS	12	6	7.50	1.00	1.00	CASP1	caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase)
UVRAG_ma	X99050	PASS	6	5.00	PASS	11	6	5.00	1.00	1.00	UVRAG	UV radiation resistance associated gene
RP3	U02556	PASS	5	6.00	PASS	12	5	6.00	1.00	1.00		RP3 candidate gene
X58528_s at	X58528_s at	PASS	5	5.20	PASS	10	5	5.20	1.00	1.00	PMP70	70kDa peroxisomal membrane protein
SFRS3	L10838	PASS	8	17.13	PASS	13	8	17.23	0.99	-1.01	SFRS3	splicing factor, arginine/serine-rich 3
MEIPEP	U29607	PASS	9	27.22	PASS	13	9	27.69	0.98	-1.02		methionine aminopeptidase

K253	D87442_at	D87442	PASS	6	8.17	PASS	9	6	8.33	0.98	-1.02	KIA0253				
CRE3	AFPX-CreX	AFPX-CreX	PASS	9	27.78	PASS	13	9	28.46	0.98	-1.02					
UBE2D3	U39318_at	U39318	PASS	8	19.00	PASS	13	8	19.54	0.97	-1.03	UBCH5C		Ubch5C		Transcript is widely expressed. Related to S. Cerevisiae UBC4 and UBC5. Closely related to human UbcH5(A) and to UbcH5B
U26312_s_at	U26312_s_at	U26312	PASS	6	5.67	PASS	12	6	5.83	0.97	-1.03			HP1Hs-gamma		similar to Drosophila heterochromatin protein HP1 Swiss-Prot Accession Number P29227, and to human heterochromatin protein HP1Hs-alpha encoded by GenBank Accession Number U26311; contains chromo domain; recognized by autoantibodies from some patients with scleroderma; heterochromatin protein
H3B	Z48950_at	Z48950	PASS	9	66.78	PASS	13	9	68.85	0.97	-1.03	H3F3B		histone H3.3		H3 histone, family 3B (H3.3B)
HNRPF	L28010_at	L28010	PASS	9	14.89	PASS	13	9	15.38	0.97	-1.03	HNRPF		HnRNP F protein		heterogeneous nuclear ribonucleoprotein F
E 23665	U90913_at	U90913	PASS	7	6.00	PASS	10	7	6.20	0.97	-1.03					
YB1	J03827_at	J03827	PASS	9	70.00	PASS	13	9	72.38	0.97	-1.03	YB1				Major histocompatibility complex, class II, Y box-binding protein I; DNA-binding protein B
ID2B	M96843_at	M96843	PASS	9	7.33	PASS	13	9	7.62	0.96	-1.04	Id2B		contractile protein		
MGC24	D14043_at	D14043	PASS	9	14.22	PASS	13	9	14.77	0.96	-1.04			MGC-24 precursor		
NDUFV3	X99728_at	X99728	PASS	8	8.63	PASS	13	8	9.00	0.96	-1.04					
MTND1	L04490_at	L04490	PASS	7	5.86	PASS	8	7	6.13	0.96	-1.05	NDUFA9		NADH dehydrogenase (ubiquinone)	12p	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9 (39kD)
STATH	U51678_at	U51678	PASS	8	10.88	PASS	13	8	11.38	0.96	-1.05			small acidic protein		
X83416_s_at	X83416_s_at	X83416	PASS	7	6.00	PASS	13	7	6.31	0.95	-1.05	PRNP		prion protein (p27-30) (Creutzfeldt-Jakob disease, Gerstmann-Strausler-Scheinker syndrome, fatal familial insomnia)	20pter-p12	prion protein (p27-30) (Creutzfeldt-Jakob disease, Gerstmann-Strausler-Scheinker syndrome, fatal familial insomnia)
UBE2L1	S81003_at	S81003	PASS	9	14.00	PASS	13	9	14.77	0.95	-1.05	UBE2L3		ubiquitin-conjugating enzyme E2L3	22q11.2	ubiquitin-conjugating enzyme E2L3
EIF2A	J02645_at	J02645	PASS	5	7.80	PASS	8	5	8.25	0.95	-1.06	EIF2A		eukaryotic translation initiation factor 2A		eukaryotic translation initiation factor 2A
DLD_ma1	L13761_ma1	L13761	PASS	9	6.67	PASS	12	9	7.08	0.94	-1.06	DLD		dihydropyrimidine dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto acid dehydrogenase complex)	7q31-q32	dihydropyrimidine dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto acid dehydrogenase complex)
OCLSF	U63717_at	U63717	PASS	7	7.00	PASS	8	7	7.50	0.93	-1.07			osteoclast stimulating factor		OSF; contains SH3 domain and ankyrin repeat
GNAO1	U01833_at	U01833	PASS	5	5.60	PASS	9	5	6.00	0.93	-1.07	NBP1		nucleotide binding protein 1 (E.coli MinD like)		nucleotide binding protein 1 (E.coli MinD like)

M63838_s_at	M63838	PASS	9	12.33	0.93	-1.07	IFI16	lq12-qter	interferon-gamma induced protein	interferon, gamma-inducible protein 16
ADD3	U37122_at	PASS	7	20.71	0.93	-1.07	ADD3	10q24.2-q24.3	adducin gamma subunit	adducin 3 (gamma)
MLL1T2	L13773_at	PASS	9	6.00	0.92	-1.08	AF-4		gamma 1 isoform of 61kDa regulatory subunit of PP2A	
Z69030_s_at	Z69030	PASS	7	12.71	0.92	-1.09				ORF1; MER37; putative transposase similar to pogo element
TIG1_xpt1	U49973_xpt1	PASS	9	7.56	0.92	-1.09				
BTKAP135	U77948_at	PASS	5	8.40	0.92	-1.09	GTF2L	7q11.23	general transcription factor II, i	general transcription factor II, i
HOU	U32849_at	PASS	9	10.00	0.92	-1.09	NMI	22q13.3	N-myc (and STAT) interactor	N-myc (and STAT) interactor
KLRB1	HG4263-HT4HG4263-H	PASS	9	14.78	0.91	-1.09				
AHNAK	M80899_at	PASS	7	18.14	0.91	-1.09	AHNAK	11q12-q13		AHNAK nucleoprotein (desmoyokin)
NA	X80909_at	PASS	9	129.22	0.91	-1.10	alpha NAC		Nascent polypeptide associated complex alpha subunit	
JAK1	M64174_at	PASS	5	8.80	0.89	-1.12	JAK1	1p32.3-p31.3	Janus kinase 1 (a protein tyrosine kinase)	Janus kinase 1 (a protein tyrosine kinase)
Z48501_s_at	Z48501	PASS	9	113.67	0.89	-1.12	PABPL1	3q22-q25	poly(A)-binding protein-like 1	poly(A)-binding protein-like 1
PRKHT31	HG2167-HT4HG2167-H	PASS	5	7.00	0.89	-1.13				
K192_MOP	D83783_at	PASS	6	6.00	0.89	-1.13	TRAP230	Xq13		thyroid hormone receptor-associated protein, 230 kDa subunit
PRF1	M31951_at	PASS	6	23.33	0.88	-1.14	PRF1	10q22		perform 1 (preforming protein)
PSMC2	D11094_at	PASS	7	9.71	0.87	-1.15	PSMC2	7q22.1-q22.3	proteasome (prosome, macropam) 26S subunit, ATPase, 2	proteasome (prosome, macropam) 26S subunit, ATPase, 2
SDHB	U17886_at	PASS	5	8.00	0.86	-1.16	sdhB		succinate dehydrogenase iron-protein subunit B	
M21119_s_at	M21119	PASS	8	59.00	0.85	-1.17				lysosomal precursor (BC 3.2.1.17)
S31125	L40397_at	PASS	9	10.78	0.84	-1.18			ribonuclease k6 precursor	ORF; putative RNase k6
RNASE6	U64998_at	PASS	6	13.33	0.84	-1.19			IK cytokine, down-regulator of HLA II	IK cytokine, down-regulator of HLA II
IK	S74221_at	PASS	8	10.13	0.84	-1.19	IK	2p15-p14		
U73477_s_at	U73477	PASS	6	6.00	0.83	-1.20			acidic nuclear phosphoprotein pp32	LANP; PHAP1; L-1pp2a
M97796_s_a	M97796	PASS	6	17.83	0.83	-1.21	ID2	2p25	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein
NIP2	U15173_at	PASS	8	4.88	0.82	-1.21	BNIP2		BCL2/adenovirus E1B 19kD-interacting protein 2	BCL2/adenovirus E1B 19kD-interacting protein 2
POLR2B	X63563_at	PASS	7	6.71	0.82	-1.22	POLR2B	4q12	polymyrase (RNA) II (DNA directed) polypeptide B (140kD)	polymyrase (RNA) II (DNA directed) polypeptide B (140kD)
AFEX-CreX	AFEX-CreX	PASS	8	15.38	0.82	-1.22				
TRAMP	X63679_at	PASS	6	8.50	0.82	-1.22	TRAM		TRAM protein	
SAP18	U96915_at	PASS	8	13.13	0.82	-1.22	SAP18		sin3 associated polypeptide p18	SAP18p
BIOC5	AFEX-BioC	PASS	9	16.00	0.82	-1.23				
RB1	HG4036-HT4HG4036-H	PASS	8	11.13	0.78	-1.29				
TFA	L06633_at	PASS	8	6.75	0.76	-1.31	HE	2	cytohesin binding protein HE	cytohesin binding protein HE
IL7R	M29696_at	PASS	8	26.38	0.76	-1.32	IL7R	5p13	interleukin 7 receptor	interleukin 7 receptor

ZFP20	HG3454-HT3	HG3454-H	PASS	7	5.43	PASS	9	7	7.22	0.75	-1.33	COPB2	3q23	coatmer protein complex, subunit beta 2 (beta prime)	coatmer protein complex, subunit beta 2 (beta prime)
COPB	X70476_at	X70476	PASS	8	6.38	PASS	13	8	8.92	0.71	-1.40				
RAP1B	HG3521-HT3	HG3521-H	PASS	9	17.56	PASS	13	9	25.62	0.69	-1.46				
BIOB3	AFFX-BioB-4	AFFX-BioB	PASS	9	27.11	PASS	13	9	39.77	0.68	-1.47				
PROGBP	Y12711_at	Y12711	PASS	6	9.33	PASS	13	6	14.00	0.67	-1.50			putative progesterone binding protein	
M27394_s at	M27394	M27394	PASS	6	6.00	PASS	11	6	9.73	0.62	-1.62			cell surface antigen B1	
DAF3	AFFX-DapX	AFFX-Dap	PASS	9	6.56	PASS	13	9	10.69	0.61	-1.63				
M14483_ma	M14483_ma	M14483	PASS	9	65.89	PASS	13	9	109.31	0.60	-1.66	PTMA	2	prothymosin, alpha (gene sequence 28)	prothymosin, alpha (gene sequence 28)
BIOB3	AFFX-BioB	AFFX-BioB	PASS	9	29.56	PASS	13	9	65.62	0.45	-2.22				

Table 2

6800 human RA Phosphatase and Kinase list

6800 human RA Phosphatase and Kinase list

name	qualifier	GeneSpring qualifier	Patients		Normals		Avg Freq - RA Patients	Avg Freq Normals	Ratio	Fold Change	Symbol	Chromoso me	Description	Kinase or Phosphatase
			called "p">4	#"P" (RA)	called "p">6	#"P" (Normal)								
Kinases														
RAC2	M64595_at	M64595	fail	3	PASS	13	3	19.85	Normal	Normal	RAC2	22q12-q13.2	ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2)	Kinase
FRAP	L34075_at	L34075	fail	1	PASS	11	1	5.73	Normal	Normal	FRAP1	1p36.2	FKBP- apamycin associated protein	Kinase
CAMKA2	U81554_at	U81554	fail	1	PASS	10	1	5.50	Normal	Normal	CAMK2G	10q22	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma	Kinase
CDK7	L20320_at	L20320	fail	1	PASS	9	1	4.89	Normal	Normal	CDK7	2p15-cen	cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase)	Kinase
EPHB4	U07695_at	U07695	fail	0	PASS	8	0	6.50	Normal	Normal	EPHB4	7	EphB4	Kinase
PRP4H	U48736_at	U48736	fail	0	PASS	8	0	5.00	Normal	Normal	PRP4		serine/threonine-protein kinase PRP4 homolog	Kinase
BLK	S76617_at	S76617	fail	0	PASS	7	0	4.71	Normal	Normal	BLK	8p23-p22	B lymphoid tyrosine kinase	Kinase
CHED	M80629_at	M80629	fail	3	PASS	10	3	5.30	Normal	Normal	CDC2L		cholinesterase-related cell division controller	Kinase
CLC	L01664_at	L01664	fail	3	PASS	9	3	7.22	Normal	Normal	CLC	19q13.1	Charot-Leyden crystal protein	Kinase
L05624 s	L05624 s_at	L05624 s	fail	3	PASS	9	3	5.56	Normal	Normal			MAP kinase kinase	Kinase
PLK	U01038_at	U01038	fail	3	PASS	9	3	5.56	Normal	Normal			pLK	Kinase
S80267 s	S80267 s_at	S80267 s	fail	4	PASS	8	4	4.88	Normal	Normal	p72syk		p72syk	Kinase
CSNK1A1	L37042_at	L37042	fail	4	PASS	7	4	8.00	Normal	Normal	CSNK1A1	13q13	casein kinase 1, alpha 1	Kinase
CSNK2A1	M55265_at	M55265	fail	3	PASS	7	3	5.86	Normal	Normal	CSNK2A1	20p13	casein kinase 2, alpha 1 polypeptide	Kinase
HG4120-H	HG4120-HT	HG4120-HT	PASS	6	fail	3	6		Disease	Disease				Kinase
LTK	D16105_at	D16105	PASS	9	fail	3	9		Disease	Disease	LTK	15	leukocyte tyrosine kinase	Kinase
K60_GNP	D31766_at	D31766	PASS	8	fail	6	8		Disease	Disease	KIAA0060		KIAA0060 gene product	Kinase
CDK2	M68520_at	M68520	PASS	8	fail	6	8		Disease	Disease	CDK2	12q13	cyclin-dependent kinase 2	Kinase
PRKACG	M34182_at	M34182	PASS	8	fail	5	8		Disease	Disease	PRKACG	9q13	protein kinase, cAMP-dependent, catalytic, gamma	Kinase
K213	D86968_at	D86968	PASS	7	fail	6	7		Disease	Disease	KIAA0213		Similar to Mouse TFIIt-associated transactivator factor p17(GB_RO-MMU11548):	Kinase
TESK1	D50863_at	D50863	PASS	5	fail	6	5		Disease	Disease	TESK1	9p13	Containing protein kinase motif	Kinase
GCDH	U69141_at	U69141	PASS	5	fail	4	5		Disease	Disease	GCDH	19p13.2	glutaryl-Coenzyme A dehydrogenase	Kinase
ILK	U40282_at	U40282	PASS	9	PASS	12	9	8.58	3.40	3.40	ILK	11p15.5-p15.4	integrin-linked kinase	Kinase
HCFC1	L20010_at	L20010	PASS	8	PASS	13	8	8.92	2.93	2.93				Kinase
PRKMK3	D87116_at	D87116	PASS	9	PASS	11	9	11.27	2.92	2.92	PRKMK3	17q11.2	protein kinase, mitogen-activated, kinase 3 (MAP kinase kinase 3)	Kinase
FAST	X86779_at	X86779	PASS	9	PASS	10	9	7.30	2.79	2.79	fast		FAST kinase	Kinase
X59932 s	X59932 s_at	X59932 s	PASS	9	PASS	13	9	22.46	2.78	2.78	CSK	15q23-q25	c-src tyrosine kinase	Kinase
CSNK2A2	M55268_at	M55268	PASS	9	PASS	7	9	6.57	2.64	2.64	CSNK2A2	16p13.3-p13.2	casein kinase 2, alpha prime polypeptide	Kinase

KL151_SPK	D63485_at	D63485	PASS	9	18.89	PASS	10	9	7.20	2.62	2.62	KIAA0151	KIAA0151 gene product	Kinase
M16750_s	M16750_s	M16750	PASS	9	34.89	PASS	13	9	13.92	2.51	2.51	PIM1	pim-1 oncogene	Kinase
RP56KA2	L07597_at	L07597	PASS	9	28.78	PASS	12	9	11.92	2.41	2.41	RP56KA1	ribosomal protein S6 kinase, 90kD, polypeptide 1	Kinase
ECGF1_ma	U62317_ma	U62317	PASS	9	66.22	PASS	13	9	27.54	2.40	2.40		arylsulfatase A	Kinase
GLA	X14448_at	X14448	PASS	9	20.56	PASS	13	9	8.62	2.39	2.39		alpha-D-galactosidase A	Kinase
DGK5Z	U51477_at	U51477	PASS	9	32.56	PASS	13	9	13.77	2.36	2.36	DGKZ	diacylglycerol kinase, zeta (104kD)	Kinase
PIM2	U77735_at	U77735	PASS	6	24.33	PASS	12	6	10.33	2.35	2.35		pim-2 protooncogene homolog pim-2h	Kinase
M54915_s	M54915_s	M54915	PASS	9	54.67	PASS	13	9	23.54	2.32	2.32		pim-1 protein	Kinase
CAKB	U43522_at	U43522	PASS	8	14.13	PASS	9	8	6.11	2.31	2.31	PTK2B	focal adhesion kinase 2 (protein kinase B)	Kinase
M13829_s	M13829_s	M13829	PASS	8	15.25	PASS	13	8	6.69	2.28	2.28	ARAF1	v-raf murine sarcoma 3611 viral oncogene homolog 1	Kinase
AKT1	M63167_at	M63167	PASS	8	23.13	PASS	11	8	10.18	2.27	2.27	AKT1	rac protein kinase-alpha	Kinase
ZAP70	L05148_at	L05148	PASS	9	36.56	PASS	13	9	16.31	2.24	2.24			Kinase
RAD23A	D21235_at	D21235	PASS	9	15.56	PASS	10	9	7.00	2.22	2.22	RAD23A	HHR23A protein, RAD23 (S, cerevisiae) homolog A	Kinase
FGR	M19722_at	M19722	PASS	9	94.78	PASS	13	9	43.00	2.20	2.20	FGR	Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog	Kinase
DAGK1	X62535_at	X62535	PASS	9	38.56	PASS	13	9	17.92	2.15	2.15	DGKA	diacylglycerol kinase	Kinase
C8FWPH	AJ000480_at	AJ000480	PASS	5	11.60	PASS	9	5	5.44	2.13	2.13	C8FW	phosphoprotein	Kinase
D63479_s	D63479_s	D63479	PASS	9	18.67	PASS	12	9	8.83	2.11	2.11	DGKD	diacylglycerol kinase, delta (130kD)	Kinase
HPK1	U66464_at	U66464	PASS	9	16.89	PASS	13	9	8.00	2.11	2.11	HPK1	hematopoietic progenitor kinase	Kinase
GPRK6	L16862_at	L16862	PASS	7	25.29	PASS	7	7	12.00	2.11	2.11	GPRK6	G protein-coupled receptor kinase 6	Kinase
IRAK1	L76191_at	L76191	PASS	9	32.67	PASS	13	9	15.54	2.10	2.10	IRAK1	interleukin-1 receptor-associated kinase 1	Kinase
PI4KB	U81802_at	U81802	PASS	7	14.71	PASS	11	7	7.00	2.10	2.10	PIK4CB	phosphatidylinositol 4-kinase, catalytic, beta polypeptide	Kinase
Z69043_s	Z69043_s	Z69043	PASS	9	57.11	PASS	13	9	27.62	2.07	2.07	H-TRAP delta	transcoen-associated protein delta subunit precursor	Kinase
GSK3A	L40027_at	L40027	PASS	9	19.89	PASS	13	9	9.77	2.04	2.04		glycogen synthase kinase 3	Kinase
PIK4	L36151_at	L36151	PASS	9	39.89	PASS	13	9	19.69	2.03	2.03	PIK4CA	phosphatidylinositol 4-kinase, catalytic, alpha polypeptide	Kinase
3PK	U09578_at	U09578	PASS	8	17.25	PASS	13	8	8.54	2.02	2.02	MAPKAPK3	mitogen-activated protein kinase-activated protein kinase 3	Kinase
MLK3	L32976_at	L32976	PASS	7	12.29	PASS	7	7	6.14	2.00	2.00	MLK3	mixed lineage kinase 3	Kinase
CLK2	L29218_at	L29218	PASS	7	13.71	PASS	11	7	7.09	1.93	1.93	CLK2	CDC-like kinase 2	Kinase
K135_PIM	D50925_at	D50925	PASS	6	12.00	PASS	9	6	6.33	1.89	1.89	KIAA0135	The KIAA0135 gene is related to pim-1 oncogene.	Kinase
ZAP112	L40399_at	L40399	PASS	6	26.50	PASS	10	6	14.00	1.89	1.89		ORF, putative	Kinase
CBOG395	D87119_at	D87119	PASS	8	19.75	PASS	12	8	10.50	1.88	1.88		GS3955	Kinase
PRKCD	D10495_at	D10495	PASS	9	30.22	PASS	12	9	16.58	1.82	1.82		protein kinase C delta-type	Kinase
CSNK1D	U29171_at	U29171	PASS	9	18.22	PASS	12	9	10.08	1.81	1.81	CSNK1D	casein kinase 1, delta	Kinase
K96_PK	D43636_at	D43636	PASS	9	15.89	PASS	13	9	9.00	1.77	1.77	KIAA0096	KIAA0096 gene product is related to a protein kinase.	Kinase
FYN	M14676_at	M14676	PASS	9	31.89	PASS	13	9	18.08	1.76	1.76	FYN	FYN oncogene related to SRC, FGR, YES	Kinase
CSNK1G2	U89896_at	U89896	PASS	6	9.83	PASS	9	6	5.67	1.74	1.74		casein kinase I gamma 2	Kinase



TRNASTL	U07424_at	U07424	PASS	7	14.00	PASS	11	7	8.09	1.73	1.73	FARSL		phenylalanine-tRNA synthetase-like	Kinase
PKUA	AB004884	AB004884	PASS	7	12.29	PASS	8	7	7.13	1.72	1.72			pKU-alpha	Kinase
U23852_s	U23852_s_at	U23852	PASS	9	66.89	PASS	13	9	38.85	1.72	1.72	lck		p56lck	Kinase
DYRK	D86550_at	D86550	PASS	9	18.67	PASS	13	9	10.85	1.72	1.72	hMNB		serine/threonine protein kinase	Kinase
SLC6A8	U36341_ma	U36341	PASS	9	13.11	PASS	9	9	7.67	1.71	1.71	SLC6A8		creatine transporter	Kinase
SSBP	M94556_at	M94556	PASS	9	23.78	PASS	13	9	14.15	1.68	1.68	SSBP		single-stranded DNA-binding protein	Kinase
D13720_s	D13720_s_at	D13720	PASS	8	14.25	PASS	13	8	8.62	1.65	1.65			ITK	Kinase
ABR	U01147_at	U01147	PASS	9	9.89	PASS	12	9	6.00	1.65	1.65	ABR		guanine nucleotide regulatory protein	Kinase
M16591_s	M16591_s_at	M16591	PASS	9	29.44	PASS	13	9	17.92	1.64	1.64	HCK		hemopoietic cell kinase	Kinase
X77588_s	X77588_s_at	X77588	PASS	8	10.88	PASS	12	8	6.67	1.63	1.63	ARD1		ARD1 N-acetyl transferase homologue	Kinase
TFE3	X97160_ma	X97160	PASS	7	9.29	PASS	7	7	6.00	1.55	1.55			TFE3 transcription factor	Kinase
M30448_s	M30448_s_at	M30448	PASS	9	58.11	PASS	13	9	38.38	1.51	1.51	CSNK2B		casein kinase 2, beta polypeptide	Kinase
K137_COS	D50927_at	D50927	PASS	8	10.25	PASS	13	8	6.85	1.50	1.50	KIAA0137		KIAA0137 gene product	Kinase
PAK1	U24152_at	U24152	PASS	9	13.22	PASS	12	9	8.83	1.50	1.50	PAK1		p21/Cdc42/Rac1-activated kinase 1 (yeast Ste20-related)	Kinase
ZPK	U07358_at	U07358	PASS	7	8.86	PASS	11	7	6.09	1.45	1.45	ZPK		serine/threonine protein kinase	Kinase
PSMB10_c	X71874_cds	X71874	PASS	9	73.89	PASS	13	9	51.23	1.44	1.44	PSMB10		proteasome (prosome, macropain) subunit, beta type, 10	Kinase
M36430_s	M36430_s_at	M36430	PASS	7	12.71	PASS	13	7	8.85	1.44	1.44	GNB1		guanine nucleotide binding protein (G protein), beta polypeptide 1	Kinase
RPS6KA2	U08316_at	U08316	PASS	5	8.00	PASS	11	5	5.64	1.42	1.42	RPS6KA3		ribosomal protein S6 kinase, 90kD, polypeptide 3	Kinase
ATP7A	AB000409_a	AB000409	PASS	9	9.89	PASS	10	9	7.10	1.39	1.39	MKNK1		MAP kinase-interacting serine/threonine kinase 1	Kinase
HG3730-HT	HG3730-HT	HG3730-HT	PASS	8	9.75	PASS	12	8	7.08	1.38	1.38			v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	Kinase
LYN	M16038_at	M16038	PASS	9	17.11	PASS	13	9	12.54	1.36	1.36	LYN		dihydrofolipamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	Kinase
D26535_s	D26535_s_at	D26535	PASS	8	10.00	PASS	11	8	7.36	1.36	1.36	DLST		dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	Kinase
DYRK2	Y09216_at	Y09216	PASS	6	10.17	PASS	12	6	7.50	1.36	1.36	DYRK2			Kinase
BTX_ma4	U78027_ma	U78027	PASS	7	10.71	PASS	12	7	7.92	1.35	1.35	FTP3		FTP3	Kinase
PSKH1	U09564_at	U09564	PASS	8	7.50	PASS	11	8	5.55	1.35	1.35	SRPK1		SFRS protein kinase 1	Kinase
VRK1	AB000449_a	AB000449	PASS	7	7.57	PASS	10	7	5.90	1.28	1.28	VRK1		vaccinia related kinase 1	Kinase
HNRNPCL	M94630_at	M94630	PASS	9	27.56	PASS	13	9	21.69	1.27	1.27	HNRPD		heterogeneous nuclear ribonucleoprotein D	Kinase
TGFB2	D50683_at	D50683	PASS	9	24.00	PASS	13	9	18.92	1.27	1.27	TGFB2		transforming growth factor, beta receptor II (70-80kD)	Kinase
GPRK5	L15388_at	L15388	PASS	6	6.33	PASS	7	6	5.00	1.27	1.27	GPRK5		G protein-coupled receptor kinase	Kinase
HG3484-HT	HG3484-HT	HG3484-HT	PASS	7	8.86	PASS	12	7	7.00	1.27	1.27				Kinase

ATM	U33841_at	U33841	PASS	5	6.20	PASS	9	5	5.11	1.21	1.21	ATM	11q22-q23	ataxia telangiectasia mutated (includes complementation groups A, C and D)	Kinase
DNAPKCS	U47077_at	U47077	PASS	7	5.29	PASS	8	7	4.38	1.21	1.21	PRKDC	8q11	DNA-dependent protein kinase catalytic subunit	Kinase
YES1	M15990_at	M15990	PASS	7	5.43	PASS	7	7	4.71	1.15	1.15	YES1	18p11.31-p11.21	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	Kinase
PRKMK1	L11284_at	L11284	PASS	7	10.29	PASS	13	7	9.46	1.09	1.09	PRKMK1	15q22.1-q22.33	protein kinase, mitogen-activated, kinase 1 (MAP kinase kinase 1)	Kinase
S203_15	L40395_at	L40395	PASS	8	6.50	PASS	9	8	6.11	1.06	1.06	SRPK2	7q22-q31.1	ORF, putative	Kinase
SRPK2	U88666_at	U88666	PASS	8	5.38	PASS	12	8	5.08	1.06	1.06	SRPK2	7q22-q31.1	SFRS protein kinase 2	Kinase
PAK3	U25975_at	U25975	PASS	5	5.60	PASS	10	5	5.40	1.04	1.04	hPAK65	1	hPAK65	Kinase
PRKACB	M34181_at	M34181	PASS	5	6.80	PASS	10	5	6.70	1.01	1.01	PRKACB	1	protein kinase, cAMP-dependent, catalytic, beta	Kinase
JAK1	M64174_at	M64174	PASS	5	8.80	PASS	13	5	9.85	0.89	-1.12	JAK1	1p32.3-p31.3	Janus kinase 1 (a protein tyrosine kinase)	Kinase

**Phosphatases**

PTPRA	M34668_at	M34668	fail	2		PASS	9	2	5.67	Normal	Normal	PTPRA	20p13	protein tyrosine phosphatase, receptor type, alpha polypeptide	Phosphatase
PTEN	U92436_at	U92436	fail	3		PASS	11	3	5.00	Normal	Normal	PTEN	10q23	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	Phosphatase
PLCD1	U09117_at	U09117	fail	4		PASS	7	4	7.57	Normal	Normal			phospholipase c delta 1	Phosphatase
PTPRE	HG620-HT6	HG620-HT6	fail	3		PASS	7	3	8.00	Normal	Normal				Phosphatase
PLCG2H	U45974_at	U45974	PASS	5	15.40	fail	0	5		Disease	Disease				Phosphatase
PTPRN	L18983_at	L18983	PASS	5	20.00	fail	0	5		Disease	Disease	PTPRN	2q35-q36.1	protein tyrosine phosphatase, receptor type, N	Phosphatase
INPPL1	L36818_at	L36818	PASS	7	21.71	fail	6	7		Disease	Disease			51C protein	Phosphatase
M33684_s	M33684_s_a	M33684	PASS	5	6.60	fail	3	5		Disease	Disease	PTPN1		non-receptor tyrosine phosphatase 1	Phosphatase
PLCB2	M95678_at	M95678	PASS	9	84.00	PASS	12	9	26.92	3.12	3.12	PLCB2	15q15	phospholipase C, beta 2	Phosphatase
K15_PPM1	D13640_at	D13640	PASS	9	29.00	PASS	12	9	11.33	2.56	2.56	KIAA0015			Phosphatase
PPP4C	X70218_at	X70218	PASS	7	27.43	PASS	11	7	11.18	2.45	2.45	PPP4C	16p12-16p11	protein phosphatase 4 (formerly X), catalytic subunit	Phosphatase
INPP5D	U57650_at	U57650	PASS	9	42.78	PASS	13	9	18.77	2.28	2.28	INPP5D	2q36-q37	SH2-containing inositol 5-phosphatase	Phosphatase
PP1	U14603_at	U14603	PASS	9	76.56	PASS	13	9	35.31	2.17	2.17	PTP4A2	1p35	protein tyrosine phosphatase type 1VA, member 2	Phosphatase
J03805_s_a	J03805_s_at	J03805	PASS	9	14.33	PASS	13	9	7.23	1.98	1.98	PPP2CB	8p12-p11.2	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	Phosphatase
M37238_s	M37238_s_a	M37238	PASS	9	11.33	PASS	9	9	6.22	1.82	1.82	PLCG2	16q24.1	phospholipase C, gamma 2 (phosphatidylinositol-specific)	Phosphatase
PTPCAAX	U48296_at	U48296	PASS	7	8.43	PASS	8	7	5.13	1.64	1.64	PTP4A1	6q12	Protein tyrosine phosphatase IVA1	Phosphatase



Table 3

HuPBMc\_RA\_U95A-Kin-PhosP.xls

Human RA PBMc data on U95

Atfy Qualifier	Atfy Name	accession	sum of Present Calls	4 of 6 present	Avg Freq RA	sum of abs present dec	7 of 13 present	Present in RA and Normal	Present in RA Absent in Normal	Avg Freq (Normal)	Fold Change RA/Normal	Name	Chromosome	Kinase or Phosphatase
<b>Kinases</b>														
446_at	CSNK1G2	U89896	6	Pass	9.17	3.54	13	Pass	TRUE	FALSE	FALSE	casein kinase 1, gamma 2; CSNK1G2	19p13.3	Kinase
490_g_at	MUTYH	U63329	6	Pass	11.00	2.97	13	Pass	TRUE	FALSE	FALSE	mutY (E. coli) homolog, p32.1	19p13.2	Kinase
41197_at	RAD23A	D21235	6	Pass	18.50	4.32	13	Pass	TRUE	FALSE	FALSE	RAD23 (S. cerevisiae) homolog A, RAD23A	19p13.2	Kinase
33300_at	CDC2L1	AL031282	6	Pass	11.83	3.76	12	Pass	TRUE	FALSE	FALSE	Human DNA sequence from clone 283E3 on chromosome 1p36.21-36.33. Contains the alternatively spliced gene for Matrix Metalloproteinase in the Female Reproductive tract MIFR1, -2, and GSSs, complete sequence.	20q11-q12	Kinase
40742_at	HCK	M16591	6	Pass	52.50	31.65	13	Pass	TRUE	FALSE	FALSE	hemopoietic cell kinase, 20q11-q12	20q11-q12	Kinase
32799_at	C1ORF2	AF023268	6	Pass	24.17	6.43	11	Pass	TRUE	FALSE	FALSE	secretory carrier membrane protein 3, mitogen-activated protein kinase kinase 3; MAP2K3	17q11.2	Kinase
1622_at	MAP2K3	D87116	6	Pass	40.17	14.39	13	Pass	TRUE	FALSE	FALSE	phosphatidylinositol 4-kinase, catalytic, beta polypeptide, PIK4CB	1q21	Kinase
146_at	PIK4CB	U81802	6	Pass	6.33	1.75	9	Pass	TRUE	FALSE	FALSE	G protein-coupled receptor kinase 6, GPRK6	5q35	Kinase
1392_at	GPRK6	L16862	4	Pass	28.25	5.50	7	Pass	TRUE	FALSE	FALSE	glutaryl Coenzyme A dehydrogenase, GCDH	19p13.2	Kinase
33314_at	GCDH	U69141	6	Pass	6.17	1.17	11	Pass	TRUE	FALSE	FALSE	KIAA0999 protein, KIAA0999	3p	Kinase
34808_at	KIAA0999	AB023216	6	Pass	12.50	2.51	13	Pass	TRUE	FALSE	FALSE	protein kinase C, delta, PRKCD	16q22.1	Kinase
32046_at	PRKCD	D10495	6	Pass	26.83	9.93	13	Pass	TRUE	FALSE	FALSE	protein kinase C, delta, PRKCD	16q22.1	Kinase
384_at	PSMB10	X71874	6	Pass	50.00	22.63	13	Pass	TRUE	FALSE	FALSE	proteasome (prosome, macropain) subunit, beta type, 10, PSMB10	12q13.3	Kinase
41249_at	UNK AL0	AL031282	6	Pass	25.67	13.23	13	Pass	TRUE	FALSE	FALSE	diacylglycerol kinase, alpha (80kD), DGKA	6p21.2	Kinase
32716_at	DGKA	X62535	6	Pass	46.33	9.56	13	Pass	TRUE	FALSE	FALSE	mitogen-activated protein kinase kinase kinase	11q13	Kinase
1779_s_at	PIM1	M16750	6	Pass	42.00	9.61	13	Pass	TRUE	FALSE	FALSE	host cell factor C1 (VPI6, accessory protein), kinase 2; MAP4K2	11q13	Kinase
31873_at	ARD1	U52112	6	Pass	8.67	2.50	11	Pass	TRUE	FALSE	FALSE	kinase 2; MAP4K2	11q13	Kinase
187_at	MAP4K2	U07349	5	Pass	5.80	1.30	7	Pass	TRUE	FALSE	FALSE	host cell factor C1 (VPI6, accessory protein), kinase 2; MAP4K2	11q13	Kinase
37910_at	HCTF1	U52112	6	Pass	8.17	3.60	11	Pass	TRUE	FALSE	FALSE	host cell factor C1 (VPI6, accessory protein), kinase 2; MAP4K2	11q13	Kinase
1780_at	FGR	M19722	6	Pass	80.83	35.22	13	Pass	TRUE	FALSE	FALSE	Gadher-Rasheed feline sarcoma viral (v-fig) oncogene homolog, FGR	11q13	Kinase
33281_at	KIAA0151	D63485	6	Pass	14.33	1.63	13	Pass	TRUE	FALSE	FALSE	IKK-related kinase epsilon, inducible IkappaB kinase, IKKE	1	Kinase
39044_s_at	DGKD	D73409	6	Pass	31.67	7.76	13	Pass	TRUE	FALSE	FALSE	diacylglycerol kinase, delta (130kD), DGKD	11q13	Kinase
40420_at	STK10	AB015718	6	Pass	35.17	8.70	13	Pass	TRUE	FALSE	FALSE	serine/threonine kinase 10, STK10	5q35.1	Kinase
40225_at	GAK	D88435	6	Pass	37.17	12.67	13	Pass	TRUE	FALSE	FALSE	cyclin G associated kinase, GAK	4p16	Kinase
632_at	GSK3A	L40027	6	Pass	19.00	5.69	13	Pass	TRUE	FALSE	FALSE	glycogen synthase kinase 3 alpha, GSK3A	5q35.1	Kinase

Human RA 2x or greater

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Affy Qualifier	Affy Name	accession	sum of Present Calls	4 of 6 present	Avg Freq RA	Std Dev RA	sum of 7 of 13 present	Present in RA and Normal	Present in RA, Absent in Normal	Absent in RA, Present in Normal	Avg Freq (Normal)	Fold Change RA / Normal	Name	Chromosome	Kinase or Phosphatase	
35796_at	PTK9L	Y17169	6	Pass	16.17	9.54	12	Pass	TRUE	FALSE	FALSE	7.42	2.18	protein tyrosine kinase 9-like (A6-related protein), PTK9L	3p21.1	Kinase
2075_s_at	MAP2K3	L36719	6	Pass	17.67	4.23	12	Pass	TRUE	FALSE	FALSE	8.00	2.21	mitogen-activated protein kinase kinase 3, MAP2K3	17q11.2	Kinase
33301_g_at	CDC2L1	AL031282	6	Pass	21.50	7.34	13	Pass	TRUE	FALSE	FALSE	9.69	2.22	Cluster Incl AL031282 Human DNA sequence from clone 28343 on chromosome 1p36.21-36.33. Contains the alternatively spliced gene for Matrix Metalloproteinase in the Female Reproductive tract		Kinase
1810_s_at	PRKCD	D10495	6	Pass	14.00	5.62	11	Pass	TRUE	FALSE	FALSE	6.27	2.23	protein kinase C, delta, PRKCD	3p	Kinase
36949_at	CSNK1D	U29171	6	Pass	45.00	11.93	13	Pass	TRUE	FALSE	FALSE	20.08	2.24	casein kinase 1, delta, CSNK1D	17q25	Kinase
1707_g_at	ARAF1	U01337	6	Pass	31.00	6.75	11	Pass	TRUE	FALSE	FALSE	13.82	2.24	v-rat murine sarcoma 3611 viral oncogene homolog 1, p11.2 ARAF1 Ser/Thr protein kinase	Xp11.4-p11.2	Kinase
38617_at	LIMK2	D45906	5	Pass	9.00	2.55	11	Pass	TRUE	FALSE	FALSE	4.00	2.25	LIM domain kinase 2, LIMK2	22q12.2	Kinase
35299_at	MKNK1	AB000409	6	Pass	8.67	2.73	12	Pass	TRUE	FALSE	FALSE	3.83	2.26	MAP kinase-interacting serine/threonine kinase 1; MKNK1		Kinase
34291_at	FARSL	U07424	6	Pass	11.00	3.35	13	Pass	TRUE	FALSE	FALSE	4.77	2.31	phenylalanine-tRNA synthetase-like; FARSL	19p13.2	Kinase
1498_at	ZAP70	L05148	6	Pass	35.67	9.71	13	Pass	TRUE	FALSE	FALSE	15.38	2.32	zeta-chain (TCR) associated protein kinase (70 kD); ZAP70	2q12	Kinase
1706_at	ARAF1	U01337	6	Pass	25.17	6.43	13	Pass	TRUE	FALSE	FALSE	10.69	2.35	v-rat murine sarcoma 3611 viral oncogene homolog 1, p11.2 ARAF1	Xp11.4-p11.2	Kinase
1127_at	RPS6KA1	L07597	6	Pass	33.67	13.82	13	Pass	TRUE	FALSE	FALSE	14.15	2.38	ribosomal protein S6 kinase, 90kD, polypeptide 1; RPS6KA1	3	Kinase
36179_at	MAPKAPK2	U12779	6	Pass	36.67	8.19	13	Pass	TRUE	FALSE	FALSE	15.31	2.40	mitogen-activated protein kinase-activated protein kinase 2; MAPKAPK2		Kinase
1652_at	PIM2	U77735	6	Pass	17.50	7.82	11	Pass	TRUE	FALSE	FALSE	7.27	2.41	pim-2 oncogene; PIM2	X	Kinase
883_s_at	PIM1	M56915	6	Pass	59.00	8.44	13	Pass	TRUE	FALSE	FALSE	24.46	2.41	pim-1 oncogene; PIM1	6p21.2	Kinase
33804_at	PTK2B	U43522	6	Pass	16.67	7.63	8	Pass	TRUE	FALSE	FALSE	6.88	2.42	protein tyrosine kinase 2 beta; PTK2B	8p21.1	Kinase
493_at	CSNK1D	U29171	6	Pass	17.17	6.43	13	Pass	TRUE	FALSE	FALSE	7.08	2.43	casein kinase 1, delta, CSNK1D	17q25	Kinase
1398_g_at	MAP3K11	L32976	6	Pass	27.83	17.62	13	Pass	TRUE	FALSE	FALSE	11.46	2.43	mitogen-activated protein kinase kinase kinase 11, MAP3K11	11q13.1-q13.3	Kinase
33903_at	DAPK3	AB007144	5	Pass	13.00	5.61	9	Pass	TRUE	FALSE	FALSE	5.22	2.49	death-associated protein kinase 3; DAPK3	19p13.3	Kinase
1134_at	ACK	L13738	6	Pass	25.00	7.07	12	Pass	TRUE	FALSE	FALSE	10.00	2.50	activated p21cdc42Hs kinase; ACK1	3	Kinase
33223_at	KIAA0561	AB011133	6	Pass	16.17	7.17	13	Pass	TRUE	FALSE	FALSE	6.46	2.50	KIAA0561 protein, KIAA0561		Kinase
32004_s_at	UNK_W32	W32483	6	Pass	10.83	5.04	13	Pass	TRUE	FALSE	FALSE	4.31	2.51			Kinase
34679_at	BCR	X02596	5	Pass	17.00	2.00	12	Pass	TRUE	FALSE	FALSE	6.67	2.55	breakpoint cluster region, BCR	22q11.23	Kinase
35365_at	ILK	U40282	6	Pass	30.17	5.98	13	Pass	TRUE	FALSE	FALSE	11.62	2.60	integrin-linked kinase, ILK	11p15.5-p15.4	Kinase

Affy Qualifier	Affy Name	accession	sum of Present Calls	4 of 6 present	Avg Freq RA	Std Dev RA	sum of abs dec	7 of 13 present	Present in RA and Normal	Present in RA, Absent in Normal	Absent in RA, Present in Normal	Avg Freq (Normal)	Fold Change RA / Normal	Name	Chromosome	Kinase or Phosphatase
38269_at	DKFZP586E0820	AL050147	6	Pass	44.67	9.63	13	Pass	TRUE	FALSE	FALSE	16.92	2.64	DKFZP586E0820 protein; DKFZP586E0820	19	Kinase
1708_s_at	CSK	X59932	6	Pass	75.50	29.19	13	Pass	TRUE	FALSE	FALSE	27.77	2.72	c-src tyrosine kinase; CSK	15q23-q25	Kinase
38003_s_at	DGKZ	U94905	6	Pass	29.17	12.50	13	Pass	TRUE	FALSE	FALSE	10.23	2.85	diacylglycerol kinase, zeta (10kD); DGKZ		Kinase
138_at	MAP4K1	U66464	6	Pass	16.33	4.13	13	Pass	TRUE	FALSE	FALSE	5.69	2.87	mitogen-activated protein kinase kinase kinase	19q13.1-q13.4	Kinase
993_at	TYK2	X54637	6	Pass	15.50	5.24	12	Pass	TRUE	FALSE	FALSE	5.25	2.95	kinase 1; MAP4K1		Kinase
40235_at	ACK	L13738	6	Pass	13.33	5.05	10	Pass	TRUE	FALSE	FALSE	3.70	3.60	tyrosine kinase 2; TYK2 activated p21cdc42Gis kinase; ACK1	19p13.2	Kinase

## Phosphatases

37384_at	KIAA0015	D13640	6	Pass	18.00	5.40	10	Pass	TRUE	FALSE	FALSE	8.80	2.05	KIAA0015 gene product; KIAA0015	22q11.22	Phosphatase
172_at	INPP5D	U57650	6	Pass	33.00	10.08	13	Pass	TRUE	FALSE	FALSE	16.08	2.05	inositol polyphosphate-5-phosphatase; INPP5D	2q36-q37	Phosphatase
41162_at	PPM1G	Y13936	6	Pass	20.00	4.05	13	Pass	TRUE	FALSE	FALSE	9.23	2.17	protein phosphatase 1G (formerly 2C); magnesium-dependent, gamma isoform; PPM1G		Phosphatase
382_at	PPP4C	X70218	6	Pass	16.83	7.36	13	Pass	TRUE	FALSE	FALSE	7.46	2.26	protein phosphatase 4 (formerly X); catalytic subunit; PPP4C	16p12-16p11	Phosphatase
210_at	PLCB2	M95678	6	Pass	49.17	20.53	12	Pass	TRUE	FALSE	FALSE	20.58	2.39	phospholipase C, beta 2; PLCB2	15q15	Phosphatase
41225_at	UNK_AL0	AL049417	6	Pass	9.17	4.88	13	Pass	TRUE	FALSE	FALSE	3.77	2.43	dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related); DUSP3	17q21	Phosphatase
794_at	PTPN6	X62055	6	Pass	28.50	11.93	13	Pass	TRUE	FALSE	FALSE	10.69	2.67	protein tyrosine phosphatase, non-receptor type 6; PTPN6	12p13	Phosphatase
1005_at	DUSP1	X68277	6	Pass	21.17	21.76	13	Pass	TRUE	FALSE	FALSE	6.46	3.28	dual specificity phosphatase 1; DUSP1	5q34	Phosphatase

37864_s_at	IGHG3	Y14737	6	Pass	93.83	76.26	13	Pass	TRUE	FALSE	FALSE	8.00	11.73	immunoglobulin heavy constant gamma 3 (G3m marker); IGHG3	14q32.33	
36482_s_at	ATP2A3	Y15724	6	Pass	17.00	5.33	12	Pass	TRUE	FALSE	FALSE	3.25	5.23	ATPase, Ca++ transporting, ubiquitous; ATP2A3	17p13.3	
40644_g_at	ITGA2B	M34480	6	Pass	37.83	9.95	11	Pass	TRUE	FALSE	FALSE	7.45	5.08	integrin, alpha 2b (platelet glycoprotein IIb or IIb/IIIa complex, antigen CD41B); ITGA2B	17q21.32	
32749_s_at	FLNA	AL050396	6	Pass	209.83	58.51	13	Pass	TRUE	FALSE	FALSE	41.46	5.06	filamin A, alpha (actin-binding protein-280); FLNA	Xq28	
33501_r_at	IGHA1	S71043	6	Pass	138.50	88.39	13	Pass	TRUE	FALSE	FALSE	28.92	4.79	immunoglobulin heavy constant alpha 1; IGH A1	14q32.33	
33822_at	NUMA1	Z11584	6	Pass	11.50	6.35	12	Pass	TRUE	FALSE	FALSE	2.42	4.76	nuclear mitotic apparatus protein 1; NUMA1	11q13	
38487_at	KIAA0246	D87433	6	Pass	35.50	24.04	8	Pass	TRUE	FALSE	FALSE	7.63	4.66	Stabilin-1		
1268_at	UBE1	M58028	6	Pass	47.50	14.10	13	Pass	TRUE	FALSE	FALSE	10.54	4.51	ubiquitin-activating enzyme E1 (A1S9T and BN75 temperature sensitivity)	Xp11.23	
37467_at	IGHD	K02882	6	Pass	25.17	37.82	10	Pass	TRUE	FALSE	FALSE	5.60	4.49	immunoglobulin heavy constant delta; IGH D	14q32.33	

Affy Qualifier	Affy Name	accession	sum of Present Calls	4 of 6 present	Avg Freq RA	Std Dev RA	sum of abs dec	7 of 13 present	Present in RA, Absent in Normal	Avg Freq (Normal)	Fold Change RA / Normal	Name	Chromosome	Kinase or Phosphatase
32378_at	PKM2	M26252	6	Pass	96.17	29.53	13	Pass	TRUE	21.77	4.42	pyruvate kinase, muscle; PKM2	15q22	
39049_at	NOTCH4	AJ243937	6	Pass	47.33	13.25	13	Pass	TRUE	11.31	4.19	Notch (Drosophila)	6p21.3	
33499_s_at	IGHA1	AF067420	6	Pass	123.33	74.06	13	Pass	TRUE	29.62	4.16	immunoglobulin heavy constant alpha 1, IGH A1	14q32.33	
36028_at	TCIRG1	U45285	6	Pass	33.17	17.12	13	Pass	TRUE	8.00	4.15	T-cell, immune regulator 1, TCIRG1	11q13.4-	
32070_at	PTPRCAP	X97267	6	Pass	119.83	16.22	13	Pass	TRUE	28.92	4.14	protein tyrosine phosphatase, receptor type, c polypeptide-associated protein, PTPRCAP	11q13.3	
32588_s_at	BRF2	X78992	6	Pass	105.50	33.35	13	Pass	TRUE	25.62	4.12	viritylate response factor 2 (EGF-response factor 2), BRF2		
37014_at	MX1	M33882	6	Pass	27.50	22.98	13	Pass	TRUE	6.69	4.11	myxovirus (influenza) resistance 1, homolog of murine (interferon-inducible protein p78), GABAR1	21q22.3	
32623_at	GABAR1	AJ225028	6	Pass	18.17	4.17	7	Pass	TRUE	4.43	4.10	gamma-aminobutyric acid (GABA) B receptor, 1, GABAR1	6p21.3	
596_s_at	CSF3R	M59820	6	Pass	40.67	20.97	12	Pass	TRUE	9.92	4.10	colony stimulating factor 3 receptor (granulocyte), CSF3R	1p35-p34.3	
1915_s_at	FOS	V01512	6	Pass	63.50	46.86	13	Pass	TRUE	15.54	4.09	v-fos FBJ murine osteosarcoma viral oncogene homolog, FOS	14q24.3	
36412_s_at	IRF7	U53831	6	Pass	17.00	10.66	12	Pass	TRUE	4.17	4.08	interferon regulatory factor 7, IRF7	11	
36138_at	CAPN4	X04106	6	Pass	57.67	25.33	13	Pass	TRUE	14.38	4.01	calpain, small polypeptide; CAPN4	19	
36879_at	ECGF1	M63193	6	Pass	89.00	78.82	12	Pass	TRUE	22.33	3.99	endothelial cell growth factor 1 (platelet-derived), ECGF1	22q13.33	
1916_s_at	FOS	V01512	6	Pass	46.17	29.96	13	Pass	TRUE	12.00	3.85	v-fos FBJ murine osteosarcoma viral oncogene homolog, FOS	14q24.3	
33273_f_at	IGL@	X57809	6	Pass	180.83	155.56	13	Pass	TRUE	47.38	3.82	immunoglobulin lambda locus, IGL @	22q11.1-q11.2	
34874_at	NTE	AJ004832	6	Pass	23.00	12.44	12	Pass	TRUE	6.08	3.78	neuropathy target esterase, NTE	19p	
41827_f_at	UNK A093	AJ032613	6	Pass	58.67	49.98	13	Pass	TRUE	15.69	3.74	SMA3, SMA3	5q13	
38647_at	COPE	AJ131182	6	Pass	44.83	17.38	13	Pass	TRUE	12.00	3.74	coatamer protein complex, subunit epsilon, COPE		
40164_at	ARHGDIA	X69550	6	Pass	42.17	14.66	13	Pass	TRUE	11.31	3.73	Rho GDP dissociation inhibitor (GDI) alpha, ARHGDIA	17q25.3	
33500_1_at	IGHA1	S71043	6	Pass	109.33	64.26	13	Pass	TRUE	30.00	3.64	immunoglobulin heavy constant alpha 1, IGH A1	14q32.33	
40718_at	CTSW	AF013611	6	Pass	30.50	19.00	10	Pass	TRUE	8.40	3.63	cathepsin W (lymphopain), CTSW	11q13.1	
33143_s_at	SLC16A3	U81800	6	Pass	43.83	23.80	13	Pass	TRUE	12.15	3.61	solute carrier family 16 (monocarboxylic acid transporters), member 3, SLC16A3	22q12.3-q13.2	
239_at	CTSD	M63138	6	Pass	76.50	38.12	13	Pass	TRUE	21.31	3.59	cathepsin D (lysosomal aspartyl protease), CTSD	11p15.5	
33816_at	UNK AF09	AF020267	6	Pass	17.33	8.45	12	Pass	TRUE	4.92	3.53	myosin IXB, MYO1B	19p13.1	
33283_at	ARRB2	AF106941	6	Pass	84.00	41.95	13	Pass	TRUE	24.00	3.50	arrestin, beta 2, ARRB2	17p13	
32750_r_at	FLNA	X53416	6	Pass	23.00	3.95	10	Pass	TRUE	6.60	3.48	filamin A, alpha (actin-binding protein-280), FLNA	Xq28	

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31874_at	GAR22	Y07846	6	Pass	15.67	5.82	12	Pass	TRUE	FALSE	FALSE	4.50	3.48	GAS2-related on chromosome 22; GAR22	22q12.2	
39997_at	PTC	AF005664	6	Pass	57.00	28.64	13	Pass	TRUE	FALSE	FALSE	16.69	3.41	proteasome P factor, complement, PTC	Xp11.3-p11.23	
41045_at	SECTM1	U77643	6	Pass	29.67	22.56	13	Pass	TRUE	FALSE	FALSE	8.69	3.41	secreted and transmembrane 1, glycoprotein Ib (platelet), GP1BB	22q11.21	
34412_s_at	GP1BB	U59632	6	Pass	85.50	35.30	13	Pass	TRUE	FALSE	FALSE	25.08	3.41	beta polypeptide, GP1BB	22q11.1	
33274_f_at	IGL@	M18645	6	Pass	162.50	133.56	13	Pass	TRUE	FALSE	FALSE	48.15	3.37	immunoglobulin lambda locus IGL@	22q11.2	
35170_at	MAN2C1	AF044414	6	Pass	21.50	5.43	10	Pass	TRUE	FALSE	FALSE	6.40	3.36	mannosidase, alpha, class 2C, member 1, MAN2C1	15q11-q13	
41168_at	TAPBP	AF029750	6	Pass	112.50	29.72	13	Pass	TRUE	FALSE	FALSE	34.00	3.31	TAP binding protein (tapasin); TAPBP	6p21.3	
37192_at	EPB49	U28389	6	Pass	56.67	18.65	12	Pass	TRUE	FALSE	FALSE	17.17	3.30	erythrocyte membrane protein band 4.9 (domain), EPB49	8p21.1	
38138_at	SI00A11	D38583	6	Pass	74.83	42.88	13	Pass	TRUE	FALSE	FALSE	22.77	3.29	SI00 calcium-binding protein A11 (calgizzanin), S100A11	1q21	
41446_f_at	RNAHP	H68340	6	Pass	25.67	13.92	13	Pass	TRUE	FALSE	FALSE	7.85	3.27	RNA helicase-related protein, RNAHP	17	
40643_at	ITGA2B	M34480	6	Pass	101.33	18.45	13	Pass	TRUE	FALSE	FALSE	31.00	3.27	integrin, alpha 2b (platelet), glycoprotein IIb of IIb/IIIa complex, antigen CD41B; ITGA2B	17q21.32	
37966_at	UNK_AA1	AA187563	6	Pass	10.17	3.43	8	Pass	TRUE	FALSE	FALSE	3.13	3.25	CGI-56 protein, CGI-56	22q13.2-q13.33	
33425_at	TIF1B	X97548	6	Pass	30.67	7.53	13	Pass	TRUE	FALSE	FALSE	9.46	3.24	KRAB-associated protein 1, TIF1B	5	
36493_at	LSP1	M33552	6	Pass	49.17	23.56	13	Pass	TRUE	FALSE	FALSE	15.31	3.21	lymphocyte-specific protein 1, LSP1	11p15.5	
34223_at	CSF3R	M59818	6	Pass	34.33	16.75	13	Pass	TRUE	FALSE	FALSE	10.69	3.21	colony stimulating factor 3 receptor (granulocyte), CSF3R	1p35-p34.3	
34780_at	PLXNB2	AB002313	6	Pass	43.67	21.77	13	Pass	TRUE	FALSE	FALSE	13.62	3.21	plexin B2, PLXNB2	22q13.33	
39649_at	ARHGAP4	X78817	6	Pass	53.00	19.42	13	Pass	TRUE	FALSE	FALSE	16.54	3.20	Rho GTPase activating protein 4, ARHGAP4	Xq28	
35786_at	KIAA0476	AB007945	6	Pass	28.33	9.29	13	Pass	TRUE	FALSE	FALSE	8.85	3.20	KIAA0476 gene product, KIAA0476	1	
39424_at	TNFRSF14	U70321	6	Pass	26.50	9.81	13	Pass	TRUE	FALSE	FALSE	8.31	3.19	tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator), TNFRSF14	1p36.3-p36.2	
1353_g_at	IL8RA	U11870	4	Pass	12.75	2.22	8	Pass	TRUE	FALSE	FALSE	4.00	3.19	interleukin 8 receptor, alpha, IL8RA	2q35	
35292_at	D6S81E	Z37166	6	Pass	29.83	5.04	13	Pass	TRUE	FALSE	FALSE	9.38	3.18	HLA-B associated transcript-1, D6S81E	6p21.3	
33438_at	WBP2	AL049981	6	Pass	59.50	19.79	13	Pass	TRUE	FALSE	FALSE	18.77	3.17	WW domain binding protein 2, WBP2	17q25	
36372_at	HK3	U51333	6	Pass	53.83	35.92	12	Pass	TRUE	FALSE	FALSE	17.00	3.17	hexokinase 3 (white cell), HK3	5q35.2	
39182_at	EMP3	U87947	6	Pass	155.83	50.34	13	Pass	TRUE	FALSE	FALSE	49.23	3.17	epithelial membrane protein 3, EMP3	19q13.3	
36229_at	IL17R	U58917	4	Pass	12.25	8.10	8	Pass	TRUE	FALSE	FALSE	3.88	3.16	interleukin 17 receptor, IL17R	22q11.1	
33371_s_at	RAB31	U59877	6	Pass	34.17	14.36	13	Pass	TRUE	FALSE	FALSE	10.85	3.15	RAB31, member RAS oncogene family, RAB31	18p11.3	
40332_at	7-60	AF109134	6	Pass	35.33	18.54	9	Pass	TRUE	FALSE	FALSE	11.22	3.15	7-60 protein, 22098	20q13.3	
810_at	ARHGEF1	U64105	6	Pass	27.83	5.49	13	Pass	TRUE	FALSE	FALSE	8.85	3.15	Rho guanine nucleotide exchange factor (GEF) 1, ARHGEF1	19q13.13	



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36960_at	EDR2	U89278	6	Pass	13.17	7.83	13	Pass	TRUE	FALSE	FALSE	4.23	3.11	early development regulator 2 (homolog of polyhormone 2); EDR2	1	
36785_at	HSPB1	Z23090	6	Pass	22.67	9.07	13	Pass	TRUE	FALSE	FALSE	7.31	3.10	heat shock 27kD protein 1; HSPB1	7q	
39082_at	ANXA6	Y00097	6	Pass	62.00	12.18	13	Pass	TRUE	FALSE	FALSE	20.15	3.08	annexin A6; ANXA6	5q32-q34	
39400_at	KIAA1055	AB028978	6	Pass	11.33	4.27	13	Pass	TRUE	FALSE	FALSE	3.69	3.07	KIAA1055 protein; KIAA1055	15	
41106_at	KCNN4	AF022797	5	Pass	10.20	5.36	9	Pass	TRUE	FALSE	FALSE	3.33	3.06	potassium intercalate/small conductance calcium-activated channel, subfamily N, member 4; KCNN4	19q13.2	
39076_s_at	DRAP1	A1991040	6	Pass	25.17	8.33	13	Pass	TRUE	FALSE	FALSE	8.23	3.06	DRI-associated protein 1 (negative cofactor 2 alpha); DRAP1	11	
39112_at	USF2	Y07661	6	Pass	15.00	4.43	13	Pass	TRUE	FALSE	FALSE	4.92	3.05	upstream transcription factor 2; c-fos interacting; USF2	19q13	
38813_at	TSC2	X75621	6	Pass	9.67	2.16	10	Pass	TRUE	FALSE	FALSE	3.20	3.02	tuberous sclerosis 2; TSC2	16p13.3	
34789_at	P16	S69272	6	Pass	23.83	10.76	13	Pass	TRUE	FALSE	FALSE	7.92	3.01	protease inhibitor 6 (placental thrombin inhibitor); P16	9p25	
37145_at	GNLY	M85276	6	Pass	111.17	70.80	13	Pass	TRUE	FALSE	FALSE	37.00	3.00	granulysin; GNLY	2p12-q11	
34707_at	CHD3	U91543	6	Pass	21.83	7.25	13	Pass	TRUE	FALSE	FALSE	7.31	2.99	chromodomain helicase DNA binding protein 3; CHD3	17p13.1	
38069_at	CLCN7	Z67743	6	Pass	29.83	6.77	11	Pass	TRUE	FALSE	FALSE	10.00	2.98	chloride channel 7; CLCN7	16p13	
38063_at	UNIK U006	U00952	6	Pass	28.17	12.42	13	Pass	TRUE	FALSE	FALSE	9.46	2.98	immunoglobulin kappa variable ID-8; IGKV1D-8	16	
37281_at	KIAA0233	D87071	6	Pass	36.33	11.18	13	Pass	TRUE	FALSE	FALSE	12.23	2.97	KIAA0233 gene product; KIAA0050	K16	
38194_s_at	IGKV1D-8	M63438	6	Pass	142.17	69.87	13	Pass	TRUE	FALSE	FALSE	47.92	2.97	immunoglobulin kappa variable ID-8; IGKV1D-8	2p12	
37411_at	KIAA0050	D30758	6	Pass	34.33	9.40	12	Pass	TRUE	FALSE	FALSE	11.58	2.96	KIAA0050 gene product; KIAA0050		
36473_at	USP20	AB023220	6	Pass	16.17	3.66	12	Pass	TRUE	FALSE	FALSE	5.50	2.94	ubiquitin specific protease 20; USP20	16p13	
36152_at	GDI1	X79353	6	Pass	47.83	11.89	13	Pass	TRUE	FALSE	FALSE	16.31	2.93	GDP dissociation inhibitor 1; GDI1	Xq28	
35530_f_at	IGL@	X92997	6	Pass	30.17	22.56	11	Pass	TRUE	FALSE	FALSE	10.36	2.91	immunoglobulin lambda locus; IGL@	22q11.1-q11.2	
40791_at	POLR2A	X63564	6	Pass	23.50	10.37	13	Pass	TRUE	FALSE	FALSE	8.08	2.91	polymerase (RNA) II (DNA directed) polypeptide A (220kD); POLR2A	17p13.1	
41753_at	ACTN4	U48734	6	Pass	30.83	12.92	13	Pass	TRUE	FALSE	FALSE	10.69	2.88	actinin, alpha 4; ACTN4	19q13	
33925_at	NRGN	X99076	6	Pass	220.17	53.81	13	Pass	TRUE	FALSE	FALSE	76.77	2.87	neurogranin (protein kinase C substrate, RC3); NRGN	11q24	
39689_at	CST3	A1362017	6	Pass	65.50	33.53	13	Pass	TRUE	FALSE	FALSE	22.85	2.87	cystatin C (amyloid angiopathy and cerebral hemorrhage); CST3	20p11.2	
1107_s_at	ISG15	M13755	6	Pass	39.67	28.62	13	Pass	TRUE	FALSE	FALSE	13.85	2.86	interferon-stimulated protein, 15 kDa; ISG15	1	
336_at	TBXA2R	D38081	5	Pass	11.80	2.59	7	Pass	TRUE	FALSE	FALSE	4.14	2.85	thromboxane A2 receptor; TBXA2R	19p13.3	
31315_at	UNK D84	D84143	5	Pass	22.00	16.09	8	Pass	TRUE	FALSE	FALSE	7.75	2.84	H1 histone family, member X; H1FX		
319_g_at	H1FX	D64142	6	Pass	86.17	25.13	13	Pass	TRUE	FALSE	FALSE	30.46	2.83	protease inhibitor 1 (anti-elastase), alpha-1-antitrypsin; PI		
36781_at	PI	X01683	6	Pass	101.67	57.50	13	Pass	TRUE	FALSE	FALSE	36.00	2.82	protease inhibitor 1 (anti-elastase), alpha-1-antitrypsin; PI	14q32.1	

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41138_at	MIC2	M16279	6	Pass	74.50	25.15	13	Pass	TRUE	FALSE	26.38	2.82	antigen identified by monoclonal antibodies 12E7, F21 and O13, MIC2	Xp22.32, Yp11.3	
41198_at	GRN	AF055008	6	Pass	69.00	41.70	11	Pass	TRUE	FALSE	24.45	2.82	granulin, GRN	17	
1294_at	UBE1L	L13852	6	Pass	22.83	3.92	10	Pass	TRUE	FALSE	8.10	2.82	ubiquitin-activating enzyme E1, like, UBE1L	3p21	
38894_g_at	NCF4	AL008637	6	Pass	18.83	7.91	13	Pass	TRUE	FALSE	6.69	2.81	neutrophil cytosolic factor 4 (NCF4), NCF4	22q13.1	
40669_s_at	CD6	U34624	4	Pass	11.00	4.76	11	Pass	TRUE	FALSE	3.91	2.81	CD6 antigen, CD6	11q13	
38671_at	KIAA0620	AB014520	6	Pass	11.00	10.24	11	Pass	TRUE	FALSE	3.91	2.81	KIAA0620 protein, KIAA0620		
38686_at	ATP6DV	X71490	6	Pass	31.17	16.81	11	Pass	TRUE	FALSE	11.09	2.81	Vacuolar proton-ATPase, subunit D, V-ATPase, subunit D, ATP6DV		
35132_at	MYOIE	X98411	6	Pass	94.33	40.45	13	Pass	TRUE	FALSE	33.62	2.81	myosin IE, MYOIE		
34405_at	USP5	U47927	6	Pass	14.00	2.68	10	Pass	TRUE	FALSE	5.00	2.80	ubiquitin specific protease 5 (uspeptidase T), USP5	12p13	
40667_at	CD6	X60992	6	Pass	31.83	11.62	13	Pass	TRUE	FALSE	11.38	2.80	CD6 antigen, CD6	11q13	
31610_at	DD96	U21049	6	Pass	21.67	9.00	12	Pass	TRUE	FALSE	7.75	2.80	epithelial protein up-regulated in carcinoma, membrane associated protein 17, DD96		
39127_f_at	PPP2R4	X73478	6	Pass	25.33	13.09	13	Pass	TRUE	FALSE	9.08	2.79	protein phosphatase 2A, regulatory subunit B (PR 53), PPP2R4	9q34	
36902_at	ARHG	X61587	6	Pass	42.67	17.57	13	Pass	TRUE	FALSE	15.31	2.79	ras homolog gene family, member G (rho G), ARHG	11p15.5-15.4	
37387_r_at	KDELRL1	X55885	6	Pass	14.17	5.56	12	Pass	TRUE	FALSE	5.08	2.79	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1, KDELRL1	19q13.3	
33535_at	P2RX1	U45448	6	Pass	9.17	4.17	10	Pass	TRUE	FALSE	3.30	2.78	purinergic receptor P2X, ligand-gated ion channel, 1, P2RX1	17p	
36940_at	TIAF1	D86970	6	Pass	5.83	1.83	10	Pass	TRUE	FALSE	2.10	2.78	TGFBI-induced anti-apoptotic factor 1, TIAF1	17	
39770_at	KIAA0250	D87437	6	Pass	8.83	3.97	11	Pass	TRUE	FALSE	3.18	2.78	KIAA0250 gene product, KIAA0250		
39119_s_at	NK4	AA631972	6	Pass	79.33	22.00	13	Pass	TRUE	FALSE	28.62	2.77	natural killer cell transcript 4, NK4	16p13.3	
41850_s_at	DIPA	U63825	6	Pass	12.33	5.39	11	Pass	TRUE	FALSE	4.45	2.77	hepatitis delta antigen-interacting protein A, 11		
36843_at	SIPA1	AB005666	6	Pass	12.83	5.67	11	Pass	TRUE	FALSE	4.64	2.77	signal-induced proliferation-associated protein 1, SIPA1	11q13.3	
38584_at	IFIT4	AF026939	6	Pass	14.33	12.68	11	Pass	TRUE	FALSE	5.18	2.77	interferon-induced protein with tetrapeptide repeats 4, IFIT4	10q24	
40955_at	UNK_U79	U79287	5	Pass	7.60	2.70	8	Pass	TRUE	FALSE	2.75	2.76	prostate tumor over expressed gene 1, PTOV1		
35653_at	GPS2	U28963	6	Pass	24.00	6.39	13	Pass	TRUE	FALSE	8.69	2.76	G protein pathway suppressor 2, GPS2		
181_g_at	UNK_S82	S82470	6	Pass	26.17	15.45	10	Pass	TRUE	FALSE	9.50	2.75	BB1-malignant cell expression-enhanced gene/tumor progression-enhanced gene (human, UM-UC-9 bladder carcinoma cell line, Rho guanine nucleotide exchange factor (GEF) 1, ARHGEF1		
38445_at	ARHGEF1	Y09160	6	Pass	24.33	6.77	13	Pass	TRUE	FALSE	8.85	2.75	Rho guanine nucleotide exchange factor (GEF) 1, ARHGEF1	19q13.13	
37992_s_at	ATP5D	A1436567	6	Pass	34.83	13.91	13	Pass	TRUE	FALSE	12.69	2.74	A1P synthase, H+ transpoting, mitochondrial F1 complex, delta subunit ATP5D		

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36780_at	CLU	M25915	6	Pass	248.17	77.71	13	Pass	TRUE	FALSE	90.46	2.74	clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2, testosterone-repressed protein message 2, adipsin-related protein complex 1, gamma 2 subunit, APIG2)	8p21-p12	
38798_s_at	G2AD	A1741833	6	Pass	16.67	3.27	13	Pass	TRUE	FALSE	6.08	2.74	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7 (18kD, B18), NDUFB7		
35773_at	NDUFB7	AA527880	6	Pass	12.33	6.35	10	Pass	TRUE	FALSE	4.50	2.74	solute carrier family 2 (facilitated glucose transporter), member 3, SLC2A3	12p13.3	
36979_at	SLC2A3	M20681	6	Pass	39.83	11.44	13	Pass	TRUE	FALSE	14.54	2.74	interferon-stimulated transcription factor 3, gamma (48kD), ISGF3G	14q11.2	
38517_at	ISGF3G	M87503	5	Pass	43.20	12.15	13	Pass	TRUE	FALSE	15.77	2.74	death-associated protein 6, DAXX	6p21.3	
41161_at	DAXX	AB015051	6	Pass	33.50	15.22	13	Pass	TRUE	FALSE	12.23	2.74	uncoupling protein 2 (mitochondrial, proton carrier), UCP2	11q13	
37591_at	UCP2	U94592	6	Pass	61.00	19.28	13	Pass	TRUE	FALSE	22.31	2.73	capping protein (actin filament), gelsolin-like; CAPG	2cen-q24	
38391_at	CAPG	M94345	6	Pass	37.00	18.49	13	Pass	TRUE	FALSE	13.54	2.73	growth factor receptor-bound protein 2, GRB2	17q24-q25	
33855_at	GRB2	M96995	6	Pass	16.17	6.97	13	Pass	TRUE	FALSE	5.92	2.73	N-sulfoglucosaminyl sulfohydrolase (sulfamidase), SGSH	17q25.3	
35026_at	SGSH	U30894	6	Pass	33.17	9.20	13	Pass	TRUE	FALSE	12.15	2.73	imidazole receptor candidate, I-1	3p21.1	
33916_at	I-1	AB023192	6	Pass	23.00	9.14	9	Pass	TRUE	FALSE	8.44	2.72	chromosome 17 open reading frame 1B, C17ORF1B	17q21	
37100_at	C17ORF1B	AJ008112	6	Pass	22.17	6.55	13	Pass	TRUE	FALSE	8.15	2.72	acetylserotonin O-methyltransferase-like, ASMTL	Xp22.3, Yp11.3	
36554_at	ASMTL	Y15521	6	Pass	14.67	7.84	7	Pass	TRUE	FALSE	5.43	2.70	CD37 antigen, CD37	19p13-q13.4	
31870_at	CD37	X14046	6	Pass	138.67	42.00	13	Pass	TRUE	FALSE	51.38	2.70	immediate early protein, ETR101	19	
41047_at	UNK_A188	A1885170	6	Pass	36.50	8.19	13	Pass	TRUE	FALSE	13.54	2.70	transportin-SR, TRN-SR	7	
36097_at	ETR101	M62831	6	Pass	105.00	35.94	13	Pass	TRUE	FALSE	39.00	2.69	methy-CpG binding domain protein 3, MBD3	19p13.3	
35813_at	TRN-SR	AA192359	6	Pass	15.17	8.38	11	Pass	TRUE	FALSE	5.64	2.69	SHC (Src homology 2 domain-containing) transforming protein 1, SHC1	1q21	
41160_at	UNK_ACO	AC005943	6	Pass	8.67	5.75	9	Pass	TRUE	FALSE	3.22	2.69	solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1, SLC25A1	22q11.21	
38118_at	SHC1	U73377	6	Pass	26.17	10.82	13	Pass	TRUE	FALSE	9.77	2.68	interferon regulatory factor 3, IRF3	19q13.3-q13.4	
38997_at	SLC25A1	X96924	6	Pass	10.17	8.04	10	Pass	TRUE	FALSE	3.80	2.68	peptidylprolyl isomerase B (cyclophilin B), PP1B	15q21-q22	
371_at	IRF3	Z50281	6	Pass	15.67	3.88	7	Pass	TRUE	FALSE	5.86	2.67	RNA binding protein; A1-rich element binding factor, SRM300	16p13.3	
35823_at	PP1B	M63573	6	Pass	75.00	22.64	13	Pass	TRUE	FALSE	28.08	2.67			
32761_at	KIAA0324	AB002322	6	Pass	35.33	7.58	13	Pass	TRUE	FALSE	13.23	2.67			

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33908_at	CAPN1	X04366	6	Pass	56.50	21.92	13	Pass	TRUE	FALSE	21.23	2.66	calpain, large polypeptide 1; CAPN1	11q13	
38597_f_at	SLC11A1	D50402	4	Pass	9.50	4.12	7	Pass	TRUE	FALSE	3.57	2.66	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1; SLC11A1	2q35	
36675_r_at	PFN1	J03191	6	Pass	174.17	57.46	13	Pass	TRUE	FALSE	65.54	2.66	profilin 1; PFN1	17p13.3	
32836_at	AGPAT1	U56417	6	Pass	25.33	2.80	13	Pass	TRUE	FALSE	9.54	2.66	1-acylglycerol-3-phosphate O-acyltransferase 1	6p21.3	
38417_at	AMPD2	M91029	6	Pass	27.00	10.08	12	Pass	TRUE	FALSE	10.17	2.66	(lysophosphatidic acid acyltransferase, alpha); adenosine monophosphate deaminase 2 (isoform 1); AMPD2	1p13.3	
39061_at	BST2	D28137	6	Pass	59.33	33.66	13	Pass	TRUE	FALSE	22.38	2.65	bone marrow stromal cell antigen 2; BST2	19p13.2	
38442_at	MFAP2	U19718	4	Pass	16.25	1.71	7	Pass	TRUE	FALSE	6.14	2.65	microfibrillar-associated protein 2; MFAP2	1p36.1-p35	
35629_at	UNK AL0	AL022238	6	Pass	23.00	12.21	11	Pass	TRUE	FALSE	8.73	2.64	ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin); RNASE2	14q24-q31	
36766_at	RNASE2	X55988	6	Pass	37.50	29.43	13	Pass	TRUE	FALSE	14.23	2.64	ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin); RNASE2	19cen-2B, member 1; MAN2B1	19cen-q13.1
41164_at	IGHM	X67301	6	Pass	134.17	51.81	13	Pass	TRUE	FALSE	51.00	2.63	immunoglobulin heavy constant mu, IGHM	14q32.33	
1693_s_at	TIMP1	D11139	6	Pass	51.50	23.10	13	Pass	TRUE	FALSE	19.62	2.63	tissue inhibitor of metalloproteinase 1 (cythroid potentiating activity, collagenase inhibitor); TIMP1	Xp11.3-p11.23	
36661_s_at	CD14	X06882	6	Pass	156.17	111.56	13	Pass	TRUE	FALSE	59.54	2.62	CD14 antigen, CD14	5q31.1	
37386_i_at	KDEL1	X55885	6	Pass	38.50	24.19	13	Pass	TRUE	FALSE	14.69	2.62	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1; KDEL1	19q13.3	
39358_at	NCOR2	U37146	6	Pass	22.17	10.13	13	Pass	TRUE	FALSE	8.46	2.62	nuclear receptor co-repressor 2; NCOR2	12q24	
31431_at	FCGRT	U12255	6	Pass	32.83	18.49	13	Pass	TRUE	FALSE	12.54	2.62	Fc fragment of IgG, receptor, transporter, alpha; FCGRT	19q13.3	
40725_at	GOSR1	AF047438	6	Pass	9.67	4.27	13	Pass	TRUE	FALSE	3.69	2.62	golgi SNAP receptor complex member 1; alpha; FCGRT	17q11	
1754_at	DAXX	AF006041	6	Pass	14.83	4.92	12	Pass	TRUE	FALSE	5.67	2.62	death-associated protein 6; DAXX	6p21.3	
37179_at	NFE2	S77763	6	Pass	15.50	8.02	13	Pass	TRUE	FALSE	5.92	2.62	nuclear factor (erythroid-derived 2); 4SKD; NFE2	12q13	
1067_at	FLT3LG	U03838	6	Pass	8.50	1.87	12	Pass	TRUE	FALSE	3.25	2.62	fms-related tyrosine kinase 3 ligand; FLT3LG	19q13.3	
38547_at	ITGAL	Y00796	6	Pass	29.33	7.63	13	Pass	TRUE	FALSE	11.23	2.61	integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polyneguide); ITGAL	16p11.2	
38730_at	KIAA0864	AB020671	6	Pass	22.50	3.94	13	Pass	TRUE	FALSE	8.62	2.61	KIAA0864 protein; KIAA0864		
33841_at	EIF5	R48209	6	Pass	10.83	3.87	12	Pass	TRUE	FALSE	4.17	2.60	knosin-like 5 (mitotic kinesin-like protein 1); KNSL5		

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503_at	POLR2L	U37690	5	Pass	41.60	10.53	13	Pass	TRUE	FALSE	16.00	2.60	polymerase (RNA) II (DNA directed) polypeptide L (7.6 kD), POLR2L	11p15	
39050_at	PABPN1	AF026029	6	Pass	24.00	7.40	13	Pass	TRUE	FALSE	9.23	2.60	poly(A)-binding protein, nuclear 1, PABPN1	14q11.2-q13	
947_at	MCM7	D55716	6	Pass	11.17	4.22	10	Pass	TRUE	FALSE	4.30	2.60	nucleosome maintenance deficient (S cerevisiae) 7, MCM7	7q21.3-q22.1	
33836_at	NPIP	AC002045	6	Pass	12.33	2.25	8	Pass	TRUE	FALSE	4.75	2.60	nuclear pore complex interacting protein, NPIP	16p13-p11	
39910_at	UNK_AA6	AA663800	6	Pass	10.17	2.64	13	Pass	TRUE	FALSE	3.92	2.59	hypothetical protein, LOC51257	1	
32091_at	UNK_ABO	AB007915	6	Pass	11.00	6.72	12	Pass	TRUE	FALSE	4.25	2.59	KIAA0446 gene product, KIAA0446	1	
11131_at	MAP2K2	L11285	6	Pass	24.83	5.19	13	Pass	TRUE	FALSE	9.62	2.58	mitogen-activated protein kinase kinase 2, MAP2K2	7q32	
40448_at	ZFP36	M92843	6	Pass	43.83	24.09	13	Pass	TRUE	FALSE	17.00	2.58	zinc finger protein homologous to Zfp-36 in mouse, ZFP36	19q13.1	
39280_at	TNRC5	U80744	6	Pass	10.50	5.32	11	Pass	TRUE	FALSE	4.09	2.57	tumour necrosis factor receptor type 1, TNRC5	1	
35674_at	PD12	AB023211	4	Pass	10.25	6.13	7	Pass	TRUE	FALSE	4.00	2.56	peptidyl arginine deiminase, type II, PD12		
198_g_at	NME3	U29656	6	Pass	22.83	6.65	13	Pass	TRUE	FALSE	8.92	2.56	non-metastatic cells 3, protein expressed in, NME3	16q13	
31812_at	GNPFR	M24470	6	Pass	19.17	7.63	12	Pass	TRUE	FALSE	7.50	2.56	guanosine monophosphate reductase, GMPR	6p23	
40296_at	UNK_AL0	AL023653	6	Pass	29.83	11.79	13	Pass	TRUE	FALSE	11.69	2.55	aminolevulinic acid, delta-synthase 2	Xp11.21	
37285_at	ALAS2	X60364	6	Pass	84.33	43.66	13	Pass	TRUE	FALSE	33.08	2.55	(sideroblastic/hypochromic anemia), ALAS2		
36994_at	ATP6C	M62762	6	Pass	60.17	24.26	13	Pass	TRUE	FALSE	23.62	2.55	ATPase, H <sup>+</sup> transporting, lysosomal (vacuolar proton pump) 16kD, ATP6C	16p13.3	
34532_at	UNK_AF0	AF035318	6	Pass	16.67	6.74	11	Pass	TRUE	FALSE	6.55	2.55	KIAA0779 protein, KIAA0779		
33251_at	KIAA0779	AB018322	6	Pass	6.50	1.76	9	Pass	TRUE	FALSE	2.56	2.54	KIAA0462 protein, KIAA0462	1	
33860_at	KIAA0462	AB007931	6	Pass	21.67	6.28	13	Pass	TRUE	FALSE	8.54	2.54	SH3 domain-containing protein 6511, LOC51165		
39437_at	UNK_Z78	Z78324	6	Pass	18.33	7.20	13	Pass	TRUE	FALSE	7.23	2.54	Ras association (RalGDS/AF-6) domain family 1, RASSF1	3p21.3	
39601_at	RDA32	AF061836	6	Pass	26.50	6.77	13	Pass	TRUE	FALSE	10.46	2.53	major histocompatibility complex, class II, DQ alpha 1, HLA-DQA1		
32773_at	HLA-DQA	AA868382	6	Pass	57.83	23.45	13	Pass	TRUE	FALSE	22.92	2.52	KIAA0670 protein/acinus, alpha 1, KIAA0670	14	
33398_at	KIAA0670	AB014570	6	Pass	29.67	13.52	9	Pass	TRUE	FALSE	11.78	2.52	metal ion homeostasis 1F (functional), MT1F	16q13	
31622_f_at	MT1F	M10943	5	Pass	29.00	15.70	11	Pass	TRUE	FALSE	11.55	2.51	transgelin 2, TAGLN2	1q21-q25	
36678_at	TAGLN2	D21261	6	Pass	175.00	42.08	13	Pass	TRUE	FALSE	69.69	2.51	cofilin 1 (non-muscle), CFL1	11q13	
33659_at	CFL1	X95404	6	Pass	207.83	56.94	13	Pass	TRUE	FALSE	82.92	2.51	ceroid-lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeier-Vogt disease), CLN3	16p12.1	
497_at	CLN3	U32680	6	Pass	18.00	5.80	11	Pass	TRUE	FALSE	7.18	2.51			

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39704_s_at	HMGY	L17131	5	Pass	20.40	4.77	7	Pass	TRUE	FALSE	FALSE	8.14	high-mobility group (nonhistone chromosomal) protein isoforms 1 and Y, HMGY	6p21	
31432_g_at	FCGRT	U12255	6	Pass	57.33	28.74	12	Pass	TRUE	FALSE	FALSE	22.92	Fe fragment of IgG, alpha FCGR1	19q13.3	
31935_s_at	UNK_U75	U75968	5	Pass	17.20	5.07	8	Pass	TRUE	FALSE	FALSE	6.88	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like helicase), DDX11	12p11	
35965_at	HSPA6	X51757	6	Pass	14.17	8.91	9	Pass	TRUE	FALSE	FALSE	2.50	heat shock 70kD protein 6 (HSP70B), HSPA6	1cen-qter	
40867_at	PPP2R1A	J02902	5	Pass	30.40	5.94	12	Pass	TRUE	FALSE	FALSE	12.17	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform, PPP2R1A		
32824_at	CLN2	AF039704	6	Pass	37.83	17.23	13	Pass	TRUE	FALSE	FALSE	15.15	ceroid-lipidosis, neuronal 2, late infantile (Gansky-Bietschowsky disease), CLN2	11p15	
40098_at	EHD1	AF001434	6	Pass	18.50	3.21	12	Pass	TRUE	FALSE	FALSE	7.42	EH domain containing 1, EHD1	11q13	
879_at	MX2	M30818	6	Pass	16.50	9.14	13	Pass	TRUE	FALSE	FALSE	6.62	myxovirus (influenza) resistance 2, homolog of murine MX2	21q22.3	
1790_s_at	CDK10	X78342	6	Pass	18.50	6.16	7	Pass	TRUE	FALSE	FALSE	7.43	cyclin-dependent kinase (CDC2-like) 10, CDK10	16q24	
411_i_at	IFITM2	X57351	6	Pass	51.67	27.91	13	Pass	TRUE	FALSE	FALSE	20.77	interferon induced transmembrane protein 2 (1-8D), IFITM2		
915_at	IFIT1	M24594	4	Pass	9.25	3.30	11	Pass	TRUE	FALSE	FALSE	3.73	interferon-induced protein 56, IFIT1	10q25-q26	
38361_g_at	RASGRP2	A1688812	6	Pass	14.50	0.84	13	Pass	TRUE	FALSE	FALSE	5.85	RAS guanyl releasing protein 2 (calcium and DAG-regulated), RASGRP2	11q13	
38631_at	TNFAIP2	M92357	6	Pass	43.83	20.08	13	Pass	TRUE	FALSE	FALSE	17.69	tumor necrosis factor, alpha-induced protein 2, TNFAIP2	14q32	
33207_at	PRKR1	A1095508	6	Pass	9.17	4.54	10	Pass	TRUE	FALSE	FALSE	3.70	protein-kinase, interferon-inducible double stranded RNA dependent inhibitor; PRKR1	13q32	
31673_s_at	CMAR	X65784	6	Pass	20.00	5.93	13	Pass	TRUE	FALSE	FALSE	8.08	cell matrix adhesion regulator, spastic paraplegia 7, paraplegin (pure and complicated autosomal recessive), PRKR1	16q, 16q24.3	
40099_at	LFP40	AB014551	6	Pass	20.00	10.20	13	Pass	TRUE	FALSE	FALSE	8.08	rho/iaa guanine nucleotide exchange factor (GEF) 2, ARHGEF2		
34206_at	KIAA0782	AB018325	6	Pass	20.17	8.66	13	Pass	TRUE	FALSE	FALSE	8.15	KIAA0782 protein, KIAA0782		
329_s_at	NUMA1	Z11584	6	Pass	18.83	5.27	13	Pass	TRUE	FALSE	FALSE	7.62	nuclear mitotic apparatus protein 1, NUMA1	11q13	
36447_at	PCNI	S80990	6	Pass	246.17	113.27	13	Pass	TRUE	FALSE	FALSE	99.69	ficollin (collagen/fibrinogen domain-containing) 1, PCNI	9q34	
41222_at	STAT6	AF067575	6	Pass	55.83	30.42	13	Pass	TRUE	FALSE	FALSE	22.62	signal transducer and activator of transcription 6, interleukin-4 induced, STAT6	12q13	

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35094_f_at	LILRA3	AF025527	6	Pass	26.00	15.35	12	Pass	TRUE	FALSE	10.58	2.46	leukocyte immunoglobulin like receptor, subfamily A (without TM domain), member 3, LILRA3	19q13.4	
33453_at	ATP6S1	AI400326	6	Pass	51.00	12.95	13	Pass	TRUE	FALSE	20.77	2.46	ATPase, H+ transporting, lysosomal (vacuolar proton pump), subunit 1, basement membrane-induced gene, ICB-1	Xq28	
41409_at	ICB-1	AF044896	6	Pass	44.67	23.90	13	Pass	TRUE	FALSE	18.23	2.45	human growth factor-regulated tyrosine kinase substrate, HGS	17q25	
33887_at	HGS	D84064	6	Pass	16.83	3.66	8	Pass	TRUE	FALSE	6.88	2.45	tissue specific transplantation antigen	8q24.3	
36936_at	TSTA3	U58766	6	Pass	10.17	1.60	13	Pass	TRUE	FALSE	4.15	2.45	P35B, TSTA3		
117_at	HSPA6	X51757	5	Pass	10.40	4.22	8	Pass	TRUE	FALSE	4.25	2.45	heat shock 70kD protein 6 (HSP70B), HSPA6		
32211_at	PSMD13	AB009398	6	Pass	10.83	7.28	7	Pass	TRUE	FALSE	4.43	2.45	proteasome (prosome, macropain) 26S subunit, non-ATPase, 13, PSMD13	11p15.5	
41337_at	AES	AF072902	6	Pass	49.67	10.39	13	Pass	TRUE	FALSE	20.31	2.45	amino-terminal enhancer of split, AES	19p13.3	
33230_at	NMP200	AJ131186	6	Pass	14.67	4.03	12	Pass	TRUE	FALSE	6.00	2.44	nuclear matrix protein NMP200 related to spleen factor PRP10, protective protein for beta-galactosidase	11q12.2	
39062_at	PPGB	AL008726	6	Pass	53.17	15.46	13	Pass	TRUE	FALSE	21.77	2.44	cytochrome b-245, alpha polypeptide, CYBA	16q24	
40609_at	UNIK A147	AI475497	6	Pass	10.50	3.45	10	Pass	TRUE	FALSE	4.30	2.44	small nuclear ribonucleoprotein 70kD polypeptide (RNP antigen), SNRP70	19q13.3	
38359_at	RASGRP2	Y12336	6	Pass	54.67	8.16	13	Pass	TRUE	FALSE	22.46	2.43	protein kinase C substrate 80K-H, PRKCSH	11q13	
35807_at	CVBA	M21186	6	Pass	218.67	86.22	13	Pass	TRUE	FALSE	89.92	2.43	arsenate resistance protein ARS2, LOC51593	19p13.1-13.2	
40875_s_at	SNRP70	X06815	6	Pass	75.00	22.68	13	Pass	TRUE	FALSE	5.08	2.43	protein kinase C substrate 80K-H, PRKCSH	7q21	
39711_at	PRKCSH	J03075	6	Pass	18.50	5.09	13	Pass	TRUE	FALSE	7.62	2.43	DKFZP586P2220 protein, H326, H326		
39832_at	LOC51593	AL096723	6	Pass	12.33	3.61	12	Pass	TRUE	FALSE	6.46	2.42	uridine phosphorylase, UP7		
40160_at	DKFZP586	AL080109	6	Pass	15.67	4.46	13	Pass	TRUE	FALSE	8.42	2.42	zinc finger protein 151 (p12-67), ZNF151		
39823_at	H326	U06631	5	Pass	20.40	5.32	12	Pass	TRUE	FALSE	8.67	2.42	KIAA0542 gene product, KIAA0542	1p36.2-136.1	
37351_at	UP	X90838	6	Pass	21.00	11.92	12	Pass	TRUE	FALSE	12.38	2.42	phosphatidylinositol transfer protein, membrane associated, PITPNM	22q12.2	
35566_f_at	UNIK AF0	AF015128	6	Pass	30.00	20.82	13	Pass	TRUE	FALSE	3.38	2.42	natural killer cell group 7 sequence, NKG7		
41532_at	ZNF151	Y09723	6	Pass	8.17	2.40	8	Pass	TRUE	FALSE	4.62	2.42	glucosidase, alpha, acid (Pompe disease, glycogen storage disease type II), GAA	17q25.2-q25.3	
36545_s_at	UNIK AB0	AB011114	6	Pass	11.17	3.31	13	Pass	TRUE	FALSE	21.92	2.42			
38297_at	PITPNM	X98654	6	Pass	53.00	15.01	13	Pass	TRUE	FALSE	39.62	2.41			
37121_at	NKG7	S69115	6	Pass	95.67	55.68	13	Pass	TRUE	FALSE	7.45	2.41			
31816_at	GAA	X55079	6	Pass	18.00	9.32	11	Pass	TRUE	FALSE					

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38029_at	MDU1	J02939	6	Pass	19.67	5.92	13	Pass	TRUE	FALSE	8.15	2.41	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2, SLC3A2	11q13	
32550_r_at	CEBPA	Y11525	6	Pass	27.00	10.02	10	Pass	TRUE	FALSE	11.20	2.41	CCAAT/enhancer binding protein (C/EBP), alpha, CEBPA	19q13.1	
33613_at	UNK_AA8	AA806239	5	Pass	8.60	1.52	7	Pass	TRUE	FALSE	3.57	2.41	paired mesoderm homeo		
40127_at	PMX1	M95929	6	Pass	16.67	5.20	13	Pass	TRUE	FALSE	6.92	2.41	box 1, PMX1	1q24	
32116_at	UNK_AB0	AB002405	6	Pass	38.50	8.89	13	Pass	TRUE	FALSE	16.00	2.41	expressed in activated T/LAK lymphocytes, LAK 4P	17q25	
41258_at	KIAA0618	N29665	6	Pass	35.50	6.25	13	Pass	TRUE	FALSE	14.77	2.40	KIAA0618 gene product, hypothetical protein FLJ10267, FLJ10267, KIAA0618		
558_at	KRT11	M98776	5	Pass	12.20	5.26	13	Pass	TRUE	FALSE	5.08	2.40	keratin 1 (epidermolytic hyperkeratosis), KRT1	12q11-q13	
40414_at	VAR52	X59303	6	Pass	20.33	4.46	13	Pass	TRUE	FALSE	8.46	2.40	valyl-tRNA synthetase 2, VAR52	6p21.3	
956_at	TUBB	X79535	6	Pass	23.00	7.13	7	Pass	TRUE	FALSE	9.57	2.40	KIAA0088 protein		
37040_at	KIAA0088	D42041	6	Pass	37.50	11.67	13	Pass	TRUE	FALSE	15.62	2.40	KIAA0088		
36161_at	ADTB2	M34175	6	Pass	18.83	7.94	13	Pass	TRUE	FALSE	7.85	2.40	adaptor-related protein complex 2, beta 1 subunit, AP2B1	17q11.2-q12	
626_s_at	IFI35	L78833	5	Pass	5.40	4.04	8	Pass	TRUE	FALSE	2.25	2.40	interferon-induced protein 35, IFI35	17q21	
36314_at	FLT3LG	U04806	6	Pass	13.50	3.67	11	Pass	TRUE	FALSE	5.64	2.40	fltn-related tyrosine kinase 3 ligand, FLT3LG	19q13.3	
36030_at	DKFZP586	AL080214	6	Pass	21.00	6.13	13	Pass	TRUE	FALSE	8.77	2.39	DKFZP586J2223 protein, DKFZP586J2223		
33833_at	SPTAN1	J05243	6	Pass	13.17	2.64	10	Pass	TRUE	FALSE	5.50	2.39	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin), SPTAN1	9q33-q34	
33813_at	TNFRSF11	AI813532	6	Pass	167.50	76.07	13	Pass	TRUE	FALSE	70.08	2.39	tumor necrosis factor receptor superfamily, member 1B; TNFRSF1B	1p36.3-p36.2	
38483_at	HSA01191	AJ011916	6	Pass	37.50	15.98	13	Pass	TRUE	FALSE	15.69	2.39	hypothetical protein; HSA011916	17p13	
33412_at	LGALS1	AI535946	6	Pass	99.50	46.06	13	Pass	TRUE	FALSE	41.77	2.38	lectin, galactoside-binding, soluble, 1 (galectin 1), LGALS1	22q13.1	
34749_at	SLC31A2	U83461	5	Pass	18.40	8.65	11	Pass	TRUE	FALSE	7.73	2.38	solute carrier family 31 (copper transporters), member 2, SLC31A2	9q31-q32	
32660_at	UNK_AB0	AB002340	6	Pass	16.67	4.23	10	Pass	TRUE	FALSE	7.00	2.38	KIAA0342 gene product, KIAA0342		
905_at	GUK1	L76200	6	Pass	46.33	17.22	13	Pass	TRUE	FALSE	19.46	2.38	guanylate kinase 1, GUK1	1q32-q41	
277_at	MCL1	L08246	6	Pass	115.17	44.97	13	Pass	TRUE	FALSE	48.38	2.38	myeloid cell leukemia sequence 1 (BCL2-related), MCL1	1q21	
922_at	PPP2R1A	J02902	6	Pass	33.50	8.36	13	Pass	TRUE	FALSE	14.08	2.38	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform, PPP2R1A		
34433_at	DOK1	AF035299	6	Pass	20.33	17.93	11	Pass	TRUE	FALSE	8.55	2.38	docking protein 1, 62kD (downstream of tyrosine kinase 1), DOK1	2p13	
1403_s_at	SCYA5	M21121	6	Pass	181.00	62.86	13	Pass	TRUE	FALSE	76.15	2.38	small inducible cytokine A5 (RANTES), SCYA5	17q11.2-q12	



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37026_at	COPEB	AF001461	6	Pass	26.50	13.94	13	Pass	TRUE	FALSE	11.15	2.38	core promoter element	10p15
1997_s_at	BAX	U19599	6	Pass	11.83	5.04	11	Pass	TRUE	FALSE	5.00	2.37	binding protein; COPEB	19q13 3-q13 4
33866_at	TPM4	X05276	6	Pass	7.33	1.63	10	Pass	TRUE	FALSE	3.10	2.37	protein; BAX	19p13 1
38051_at	MAL	X76220	6	Pass	31.83	15.48	13	Pass	TRUE	FALSE	13.46	2.36	mal, 1-cell differentiation protein, MAL	2cen-q13
1347_at	CDC25B	S78187	6	Pass	33.83	10.44	13	Pass	TRUE	FALSE	14.31	2.36	cell division cycle 25B, CDC25B	20p13
36603_at	GCN1L1	D86973	6	Pass	14.00	2.61	13	Pass	TRUE	FALSE	5.92	2.36	GCN1 (general control of amino-acid synthesis 1, yeast)-like 1, GCN1L1	12q24 2
36058_at	DKFZP586A1096741		6	Pass	14.33	2.42	13	Pass	TRUE	FALSE	6.08	2.36	hypothetical protein, DKFZP586O0223	22
40196_at	HYA22	D88153	5	Pass	10.40	3.65	12	Pass	TRUE	FALSE	4.42	2.35	HYA22 protein, ILYA22	3p21 3
33361_at	GNG3LG	AF052149	6	Pass	14.67	2.66	13	Pass	TRUE	FALSE	6.23	2.35	guanine nucleotide binding protein (G protein), gamma 3, linked,	q13 5
34491_at	OASL	AJ225089	6	Pass	7.33	5.39	8	Pass	TRUE	FALSE	3.13	2.35	2'-5'-oligoadenylate synthetase-like, OASL	12q24 2
41165_g_at	IGHM	X67201	6	Pass	150.00	56.88	13	Pass	TRUE	FALSE	63.92	2.35	immunoglobulin heavy constant mu, IGHM	14q32 33
31504_at	HDLBP	M64098	6	Pass	13.67	4.68	12	Pass	TRUE	FALSE	5.83	2.34	high density lipoprotein binding protein (vlgm), HDLBP	2q37
1237_at	IER3	S81914	5	Pass	10.40	5.32	9	Pass	TRUE	FALSE	4.44	2.34	immediate early response 3, IER3	6p21 3
38117_at	SEC24C	D38555	6	Pass	15.67	3.44	10	Pass	TRUE	FALSE	6.70	2.34	SEC24 (S. cerevisiae) related gene family, member C, SEC24C	10
38423_at	UNK_L389	L38935	6	Pass	36.50	12.47	13	Pass	TRUE	FALSE	15.62	2.34		
38064_at	LRP	X79882	6	Pass	23.17	10.70	13	Pass	TRUE	FALSE	9.92	2.33		
39158_at	ATF5	AB021663	6	Pass	7.00	3.58	10	Pass	TRUE	FALSE	3.00	2.33	activating transcription factor 5, ATF5	
39597_at	KIAA0843	AB020650	6	Pass	10.50	4.97	12	Pass	TRUE	FALSE	4.50	2.33	KIAA0843 protein, KIAA0843	
34695_at	GA17	AB16724	6	Pass	30.67	18.23	13	Pass	TRUE	FALSE	13.15	2.33	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2, SMARCD2	17q23-q24
39994_at	CCR1	D10925	5	Pass	17.60	14.91	9	Pass	TRUE	FALSE	7.56	2.33	chemokine (C-C motif) receptor 1, CCR1	3p21
37799_at	ASGR2	X55284	6	Pass	13.33	6.31	11	Pass	TRUE	FALSE	5.73	2.33	asialoglycoprotein receptor 2, ASGR2	17p
4905_s_at	IL11RA	U32324	6	Pass	9.67	3.20	13	Pass	TRUE	FALSE	4.15	2.33	interleukin 11 receptor, alpha, IL11RA	9p13
849_g_at	UNK_U19	U19261	6	Pass	10.00	2.45	13	Pass	TRUE	FALSE	4.31	2.32	TNF receptor-associated factor 1, TRAF1	9q33-q34
34691_f_at	ARPC4	AF006087	6	Pass	25.00	6.63	13	Pass	TRUE	FALSE	10.77	2.32	actin related protein 2/3 complex, subunit 4 (20 kD), ARPC4	
35244_at	KIAA0460	AB007929	5	Pass	11.60	3.65	11	Pass	TRUE	FALSE	5.00	2.32	KIAA0460 protein, KIAA0460	1
32336_at	ALDOA	X05246	6	Pass	129.33	37.93	13	Pass	TRUE	FALSE	55.77	2.32	aldolase A, fructose-bisphosphate, ALDOA	16q22-q24
33838_at	D6S52E	M33519	6	Pass	30.67	4.37	13	Pass	TRUE	FALSE	13.23	2.32	HLA-B associated transcript-3, D6S52E	6p21 3
40885_s_at	UNK_N30	N30151	6	Pass	18.33	2.58	13	Pass	TRUE	FALSE	7.92	2.31	eukaryotic translation initiation factor 4B, EIF4B	
38893_at	NCF4	AL008637	6	Pass	55.17	27.67	13	Pass	TRUE	FALSE	23.85	2.31	neutrophil cytosolic factor 4 (40kD), NCF4	22q13 1

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40365_at	GNAI5	M63904	6	Pass	15.83	7.47	13	Pass	TRUE	FALSE	6.85	2.31	guanine nucleotide binding protein (G protein), alpha 15 (Gq class); GNAI5	19p13.3	
39795_at	CLAPM1	D63475	6	Pass	80.00	25.55	13	Pass	TRUE	FALSE	34.62	2.31	adaptor-related protein complex 2, mu 1 subunit, AP2M1	3q28	
38729_at	FKBP4	M88279	6	Pass	11.17	3.06	12	Pass	TRUE	FALSE	4.83	2.31	FK506-binding protein 4 (59kD), FKBP4		
39385_at	ANPEP	M22324	6	Pass	16.50	5.75	7	Pass	TRUE	FALSE	7.14	2.31	alanine aminopeptidase (aminopeptidase N, aminopeptidase M, microsomal)	15q25-q26	
37298_at	GABARAP	AF044671	6	Pass	123.67	48.80	13	Pass	TRUE	FALSE	53.54	2.31	aminopeptidase, CD13, p150, ANPEP	17	
2019_s_at	ITGB7	M68892	6	Pass	13.50	6.35	13	Pass	TRUE	FALSE	5.85	2.31	GABA(A) receptor-associated protein, GABARAP		
36035_at	GPAAL	AB002135	6	Pass	24.33	6.83	13	Pass	TRUE	FALSE	10.54	2.31	integrin, beta 7, ITGB7 glycoposphatidylinositol anchor attachment 1, GPAAL	12q13.13	
37796_at	UNK_AF0	AF053356	6	Pass	28.33	2.94	11	Pass	TRUE	FALSE	12.27	2.31	leucine-rich neuronal protein, LRN	7q22	
32174_at	SLC9A3R1	AF015926	6	Pass	29.83	5.27	13	Pass	TRUE	FALSE	12.92	2.31	solute carrier family 9 (sodium/hydrogen exchange), isoform 3 regulatory factor 1, SLC9A3R1		
36322_at	FUT7	AB012668	4	Pass	10.00	3.46	9	Pass	TRUE	FALSE	4.33	2.31	fructosyltransferase 7 (alpha 1,3) fructosyltransferase, FUT7	9	
38091_at	LGALS9	Z49107	6	Pass	60.00	23.87	13	Pass	TRUE	FALSE	26.00	2.31	lectin, galactoside-binding, soluble, 9 (gallectin 9), LGALS9		
33706_at	SART1	AB006198	6	Pass	19.50	4.72	13	Pass	TRUE	FALSE	8.46	2.30	squamous cell carcinoma antigen recognised by 1 cells, SART1		
1919_at	VAV1	X16316	4	Pass	13.25	3.77	8	Pass	TRUE	FALSE	5.75	2.30	xen 1 oncogene, VAV1	19p13.2	
39053_at	HPRP3P	AF016370	6	Pass	6.33	1.63	8	Pass	TRUE	FALSE	2.75	2.30	U4/U6-associated RNA splicing factor, HPRP3P	1q21.1	
880_at	FKBP1A	M34539	6	Pass	59.33	20.33	13	Pass	TRUE	FALSE	25.77	2.30	FK506-binding protein 1A (12kD), FKBP1A	20p13	
37947_at	KIAA0043	D26362	6	Pass	16.50	8.46	12	Pass	TRUE	FALSE	7.17	2.30	KIAA0043 gene product, KIAA0043		
37376_at	LOC51035	M68864	6	Pass	28.33	9.73	13	Pass	TRUE	FALSE	12.31	2.30	ORF, LOC51035		
32218_at	UNK_AF0	AF034176	6	Pass	31.67	11.67	13	Pass	TRUE	FALSE	13.77	2.30			
41460_at	SIP	AF080561	6	Pass	9.00	3.95	12	Pass	TRUE	FALSE	3.92	2.30	SVT1 interacting protein, SIP		
35749_at	TADA3L	AF069733	6	Pass	44.00	13.48	13	Pass	TRUE	FALSE	19.15	2.30	transcriptional adaptor 3 (ADA3, yeast homolog)-like (PCAF histone acetylase complex), TADA3L		
38710_at	UNK_AL0	AL096714	6	Pass	29.67	8.82	13	Pass	TRUE	FALSE	12.92	2.30	hypothetical protein FLJ20113, FLJ20113		
41386_1_at	KIAA0346	AB002344	6	Pass	16.83	5.60	12	Pass	TRUE	FALSE	7.33	2.30	KIAA0346 protein, KIAA0346	17p13.1	
344_s_at	CNP	D13146	5	Pass	22.60	8.26	13	Pass	TRUE	FALSE	9.85	2.30	basigin, BSG		
36162_at	BSG	X64364	6	Pass	18.00	2.28	13	Pass	TRUE	FALSE	7.85	2.29	carboxy terminal LIM domain protein 1, CLIM1	19p13.3	
36937_s_at	CLIM1	U90878	6	Pass	18.17	6.40	13	Pass	TRUE	FALSE	7.92	2.29		10qter	

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1158_s_at	CALM3	J04046	6	Pass	22.50	4.04	11	Pass	TRUE	FALSE	FALSE	9.82	calmodulin 3 (phosphorylase kinase, delta), CALM3	19q13.2-q13.3	
38976_at	CORO1A	D44497	6	Pass	230.67	59.84	13	Pass	TRUE	FALSE	FALSE	100.77	coronin, actin-binding protein 1A, CORO1A		
39722_at	NCOR1	AF044209	6	Pass	17.17	8.80	10	Pass	TRUE	FALSE	FALSE	7.50	nuclear receptor co-repressor 1, NCOR1	17p11.2	
32909_at	AQP5	U46569	6	Pass	11.67	3.50	10	Pass	TRUE	FALSE	FALSE	5.10	aquaporin 5, AQP5	12q13	
932_1_at	ZNF91	L11672	6	Pass	19.17	9.22	13	Pass	TRUE	FALSE	FALSE	8.38	zinc finger protein 91 (HPF7, HTF10), ZNF91	19p13.1-p12	
39908_at	PAF65A	AF069735	6	Pass	111.50	49.03	9	Pass	TRUE	FALSE	FALSE	48.78	PCAF associated factor 65 alpha, PAF65A		
31638_at	NDUF57	AC005329	6	Pass	20.00	8.15	8	Pass	TRUE	FALSE	FALSE	8.75	latent transforming growth factor beta binding protein 4, LTBP4	19q13.1-q13.2	
33137_at	LTBP4	Y13622	6	Pass	12.00	2.90	12	Pass	TRUE	FALSE	FALSE	5.25	latent transforming growth factor beta binding protein 4, LTBP4		
39343_at	HSU53209	AW026656	6	Pass	7.17	4.12	7	Pass	TRUE	FALSE	FALSE	3.14	transformer-2 alpha (htr-a-2 alpha); HSU53209		
32370_at	GZMB	M57888	6	Pass	46.83	29.69	13	Pass	TRUE	FALSE	FALSE	20.54	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1), GZMB	14q11.2	
816_g_at	DOK1	U70987	6	Pass	30.17	18.29	13	Pass	TRUE	FALSE	FALSE	13.23	docking protein 1, 62kD (downstream of tyrosine kinase 1), DOK1	2p13	
32658_at	UNK_AL0	AL031228	6	Pass	10.33	2.25	13	Pass	TRUE	FALSE	FALSE	4.54	biomodomain-containing 2, BRD2	6p21.3	
36208_at	FSRG1	D42040	6	Pass	20.83	4.36	13	Pass	TRUE	FALSE	FALSE	9.15	solute carrier family 25 (mitochondrial carrier, carnitine transporter), member 1, SLC25A1	22q11.21	
38998_g_at	SLC25A1	X06024	6	Pass	11.83	3.82	10	Pass	TRUE	FALSE	FALSE	5.20	myeloid cell leukemia sequence 1 (BCL2-related), MCL1	1q21	
33146_at	MCL1	L08246	6	Pass	116.17	36.29	13	Pass	TRUE	FALSE	FALSE	51.08	myeloid cell leukemia sequence 1, LYLL		
402_s_at	ICAM3	X69819	6	Pass	46.33	18.16	13	Pass	TRUE	FALSE	FALSE	20.38	intercellular adhesion molecule 3, ICAM3	19p13.3-p13.2	
39971_at	LYL1	M22637	6	Pass	13.83	3.54	11	Pass	TRUE	FALSE	FALSE	6.09	lymphoblastic leukemia derived sequence 1, LYLL	19p13.2	
32646_at	KIAA0449	AB007918	5	Pass	22.20	3.56	9	Pass	TRUE	FALSE	FALSE	9.78	KIAA0449 protein, KIAA0449	1	
31901_at	KCNAB2	AF044253	6	Pass	28.50	8.12	9	Pass	TRUE	FALSE	FALSE	12.56	potassium voltage-gated channel, shaker-related subfamily, beta member 2, KCNAB2	1p36.3	
40147_at	VATI	U18009	6	Pass	14.83	5.74	13	Pass	TRUE	FALSE	FALSE	6.54	membrane protein of cholinergic synaptic vesicles, VAT1	17q21	
40130_at	FSTL1	U06863	6	Pass	17.00	5.66	12	Pass	TRUE	FALSE	FALSE	7.50	folistatin-like 1, FSTL1	7q21.2-q31.1	
151_s_at	UNK_V001	V00599	6	Pass	42.17	11.99	13	Pass	TRUE	FALSE	FALSE	18.62	tubulin, beta polypeptide, TUBB	6p21.3	
766_at	LGALS9	AB006782	6	Pass	31.33	14.72	13	Pass	TRUE	FALSE	FALSE	13.85	lectin, galactoside-binding, soluble, 9 (galactin 9), LGALS9		
33863_at	ORP150	U65785	6	Pass	25.50	5.61	11	Pass	TRUE	FALSE	FALSE	11.27	oxygen regulated protein (150kD), ORP150	11	
41728_at	KIAA0152	D63486	6	Pass	19.83	5.00	13	Pass	TRUE	FALSE	FALSE	8.77	KIAA0152 gene product; KIAA0152	12	
37307_at	GNAI2	X04828	6	Pass	147.67	57.65	13	Pass	TRUE	FALSE	FALSE	65.31	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2, GNAI2	3p21	

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33826_at	CIZ1	AL120500	6	Pass	21.83	3.97	12	Pass	TRUE	FALSE	9.67	2.26	Cipl-interacting zinc finger protein, CIZ1	9q34.1	
1795_g_at	CCND3	M92287	6	Pass	94.50	24.91	13	Pass	TRUE	FALSE	41.85	2.26	cyclin D3, CCND3	6p21	
38674_at	IGFBP6	AA115140	6	Pass	103.50	49.49	13	Pass	TRUE	FALSE	45.85	2.26	hypothetical protein FLJ10262, FLJ10262	9	
39423_f_at	SPOP	AJ000644	6	Pass	12.50	7.74	11	Pass	TRUE	FALSE	5.55	2.25	speckle-type POZ protein, SPOP		
39133_at	GCN5L1	AI525379	5	Pass	7.00	2.00	9	Pass	TRUE	FALSE	3.11	2.25	GCN5 (general control of amino-acid synthesis, yeast, homolog)-like 1, GCN5L1	12q13-q14	
34224_at	KIAA0954	AC004770	6	Pass	4.67	3.33	13	Pass	TRUE	FALSE	2.08	2.25	retinoid X receptor, alpha	9q34.3	
32800_at	RXRA	U66306	6	Pass	56.33	25.13	13	Pass	TRUE	FALSE	25.08	2.25	RXRA		
33232_at	CRIP1	AI017574	6	Pass	73.33	19.72	13	Pass	TRUE	FALSE	32.69	2.24	cysteine-rich protein 1 (intestinal), CRIP1	7q11.23	
33352_at	H2BFO	X57985	6	Pass	29.67	10.27	13	Pass	TRUE	FALSE	13.23	2.24	H2B histone family, member Q; H2BFO	14q21-q23	
38724_at	KIAA0515	AB011087	6	Pass	10.17	1.83	13	Pass	TRUE	FALSE	4.54	2.24	KIAA0515 protein, KIAA0515		
1505_at	TYMS	D00596	5	Pass	7.00	2.00	8	Pass	TRUE	FALSE	3.13	2.24	thymidylate synthetase, TYMS	18p11.32	
36984_f_at	HPR	X89214	5	Pass	7.00	2.83	8	Pass	TRUE	FALSE	3.13	2.24	haploglobin-haploglobin-related protein HP, HPR	16q22.1	
35302_at	TAP	AJ132712	6	Pass	53.50	14.82	13	Pass	TRUE	FALSE	23.92	2.24	nuclear RNA export factor 1 (Mex67, yeast, homolog), NXF1		
36996_at	OS-9	U41635	6	Pass	66.00	19.85	13	Pass	TRUE	FALSE	29.54	2.23	amplified in osteosarcoma, OS-9	12q13	
38672_at	PPP1R10	Y13247	6	Pass	22.83	7.78	13	Pass	TRUE	FALSE	10.23	2.23	protein phosphatase 1, regulatory subunit 10, PPP1R10	6p21.3	
41189_at	TNFRSF12	Y09392	6	Pass	11.50	4.18	13	Pass	TRUE	FALSE	5.15	2.23	tumor necrosis factor receptor superfamily, member 12 (translocating chain-association membrane protein), TNFRSF12	1p36.2	
38432_at	ISG15	AA203213	6	Pass	16.50	13.82	10	Pass	TRUE	FALSE	7.40	2.23	interferon-stimulated protein, 15 kDa, ISG15	1	
38279_at	GNAZ	D90150	6	Pass	11.83	4.62	13	Pass	TRUE	FALSE	5.31	2.23	guanine nucleotide binding protein (G protein), alpha 2 polypeptide, GNAZ	22q11.22	
38585_at	HBG2	M91036	6	Pass	101.50	94.05	12	Pass	TRUE	FALSE	45.58	2.23	hemoglobin, gamma A, hemoglobin, gamma G, HBG1, HBG2	1p15.5	
38112_g_at	CSPG2	X15998	6	Pass	69.67	52.00	13	Pass	TRUE	FALSE	31.31	2.23	chondroitin sulfate proteoglycan 2 (versican), CSPG2	5q14.3	
1274_s_at	CDC34	L22005	6	Pass	10.17	3.25	7	Pass	TRUE	FALSE	4.57	2.22	cell division cycle 34, CDC34	19p13.3	
1643_g_at	MTA1	U35113	6	Pass	8.00	2.19	10	Pass	TRUE	FALSE	3.60	2.22	metastasis associated 1, MTA1		
243_g_at	MAP4	M64571	6	Pass	10.00	3.63	10	Pass	TRUE	FALSE	4.50	2.22	microtubule-associated protein 4, MAP4	3p21	
37346_at	ARF5	M57567	6	Pass	46.67	18.51	12	Pass	TRUE	FALSE	21.00	2.22	ADP-ribosylation factor 5, ARF5	7q31.3	
37959_at	KIAA0154	D63876	6	Pass	20.00	7.38	13	Pass	TRUE	FALSE	9.00	2.22	KIAA0154 protein, ADP-ribosylation factor binding protein GGA3, KIAA0154	17	
38663_at	BCRP1	A1033692	6	Pass	23.50	7.23	12	Pass	TRUE	FALSE	10.58	2.22	Breakpoint cluster region protein, uterine leiomyoma, 1, barrier to autointegration factor, BCRP1	14q24.1	

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37844_at	UNIK_A126	AI263885	6	Pass	20.67	8.87	13	Pass	TRUE	FALSE	FALSE	9.31	2.22	class I cytokine receptor; WSX-1	19p13.11	
32607_at	BASP1	AF039656	6	Pass	36.33	21.37	13	Pass	TRUE	FALSE	FALSE	16.38	2.22	brain acid-soluble protein 1, BASP1	5p14-15	
33396_at	GSTP1	U12472	6	Pass	70.17	32.53	13	Pass	TRUE	FALSE	FALSE	31.69	2.21	glutathione S-transferase p1, GSTP1	11q13	
39330_s at	ACTN1	M95178	6	Pass	15.83	5.12	13	Pass	TRUE	FALSE	FALSE	7.15	2.21	actinin, alpha 1; ACTN1	14q24	
38703_at	UNIK_AF0	AF005050	6	Pass	16.17	4.07	13	Pass	TRUE	FALSE	FALSE	7.31	2.21	aspartyl aminopeptidase; DSNPEP		
40723_at	SIT	AJ010059	6	Pass	16.17	4.62	13	Pass	TRUE	FALSE	FALSE	7.31	2.21	SHP2 interacting transmembrane adaptor, SIT		
464_s at	IFI35	U72882	6	Pass	16.17	8.98	13	Pass	TRUE	FALSE	FALSE	7.31	2.21	interferon-induced protein 35, IFI35	17q21	
32226_at	MAP4	M64571	6	Pass	12.67	4.72	11	Pass	TRUE	FALSE	FALSE	5.73	2.21	microtubule-associated protein 4, MAP4	3p21	
868_at	TAF2H	U13991	6	Pass	33.33	7.76	13	Pass	TRUE	FALSE	FALSE	15.08	2.21	TATA box binding protein (TBP)-associated factor, RNA polymerase II, h. 30kD, TAF2H	11p15.3	
38056_at	KIAA0195	D83779	6	Pass	17.33	4.55	13	Pass	TRUE	FALSE	FALSE	7.85	2.21	KIAA0195 gene product, KIAA0195	17	
37898_r at	TFE3	AJ985964	4	Pass	37.00	14.72	8	Pass	TRUE	FALSE	FALSE	16.75	2.21	neofol factor 3 (intestinal); TFE3	21q22.3	
654_at	MXII	L07648	6	Pass	14.17	7.36	12	Pass	TRUE	FALSE	FALSE	6.42	2.21	MAX-interacting protein 1, MXII	10q24-q25	
33602_at	EDG6	AJ000479	6	Pass	27.17	6.34	13	Pass	TRUE	FALSE	FALSE	12.31	2.21	endothelial differentiation, G-protein-coupled receptor 6, EDG6	19p13.3	
39308_r at	UNIK_X81	X81637	6	Pass	9.67	2.88	13	Pass	TRUE	FALSE	FALSE	4.38	2.20	clathrin, light polypeptide (Leb), CLTB	4q2-q3	
37904_s at	GNL1	X66436	6	Pass	6.17	1.33	10	Pass	TRUE	FALSE	FALSE	2.80	2.20	ras homolog gene family, member C, ARHC	1p21-p13	
1395_at	ARHC	L25081	5	Pass	13.00	7.11	11	Pass	TRUE	FALSE	FALSE	5.91	2.20	glucose phosphate isomerase; GPI	19q13.1	
39122_at	GPI	K03515	6	Pass	33.00	7.87	13	Pass	TRUE	FALSE	FALSE	15.00	2.20	metallothionein 1B (functional), MT1B	16q13	
609_f at	MT1B	M13485	4	Pass	27.00	5.72	11	Pass	TRUE	FALSE	FALSE	12.27	2.20	ribosomal protein L23-like, RPL23L	11p15.5	
34358_at	RPL23L	Z49254	6	Pass	22.67	6.38	13	Pass	TRUE	FALSE	FALSE	10.31	2.20	glutamate receptor, metabotropic 4, GRM4	6p21.3	
35485_at	GRM4	X80818	5	Pass	53.40	13.24	7	Pass	TRUE	FALSE	FALSE	24.29	2.20	sphingomyelin phosphodiesterase 1, acid lysosomal (acid sphingomyelinase), SMPD1	11p15.4-p15.1	
32574_at	SMPD1	X59960	6	Pass	13.17	4.17	13	Pass	TRUE	FALSE	FALSE	6.00	2.19	synaptobinding protein 2; STXBP2	19p13.3-p15.2	
38259_at	STXBP2	AB002559	6	Pass	12.50	4.32	10	Pass	TRUE	FALSE	FALSE	5.70	2.19	acyl-Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme A thiolase), ACAA1	3p23-p22	
36417_s at	UNIK_AF0	AF035295	6	Pass	15.17	5.23	12	Pass	TRUE	FALSE	FALSE	6.92	2.19	hypothetical protein FLJ20386, FLJ20386		
35154_at	UNIK_W68	W68046	6	Pass	52.33	10.75	8	Pass	TRUE	FALSE	FALSE	23.88	2.19	S100 calcium-binding protein A4 (calcium protein, calyculin, mclastasin, mune placental homolog), S100A4	1q21	
38087_s at	S100A4	W72186	6	Pass	177.67	62.89	13	Pass	TRUE	FALSE	FALSE	81.08	2.19			

Affy Qualifier	Affy Name	accession	sum of Present Calls	4 of 6 present	Avg Freq RA	Std Dev RA	sum of abs dec	7 of 13 present	Present in RA and Normal	Present in RA, Absent in Normal	Absent in RA, Present in Normal	Avg Freq (Normal)	Fold Change	Name	Chromosome	Phosphatase
1583_at	TNFRSF1B	M32315	6	Pass	92.83	44.60	13	Pass	TRUE	FALSE	FALSE	42.38	2.19	tumor necrosis factor receptor superfamily, member 1B; TNFRSF1B	1p36.3-p36.2	
214_at	MSX1	M97676	5	Pass	10.40	4.51	8	Pass	TRUE	FALSE	FALSE	4.75	2.19	msx (Drosophila) homeo box homolog 1 (formerly homeo box 7); MSX1	4p16.3-p16.1	
38789_at	TKT	L12711	6	Pass	97.00	62.34	13	Pass	TRUE	FALSE	FALSE	44.31	2.19	homeo box 7; MSX1	3p14.3	
40106_at	E1B-AP5	A1007509	6	Pass	32.83	11.87	13	Pass	TRUE	FALSE	FALSE	15.00	2.19	transketolase (Wernicke-Korsakoff syndrome); E1B-55kDa-associated protein 5; E1B-AP5		
38831_f_at	UNK_AF0	AF053356	6	Pass	67.17	23.27	13	Pass	TRUE	FALSE	FALSE	30.69	2.19	guanine nucleotide binding protein (G protein), beta polypeptide 2; GNB2	7q21.3-q22.1	
1804_at	KLK3	X07730	6	Pass	6.33	1.51	10	Pass	TRUE	FALSE	FALSE	2.90	2.18	kallikrein 3, prostate specific antigen; KLK3	19q13	
38735_at	KIAA0513	AB011085	6	Pass	24.33	8.55	13	Pass	TRUE	FALSE	FALSE	11.15	2.18	KIAA0513 gene product; KIAA0513		
41443_at	TIC	U63127	6	Pass	25.67	6.02	13	Pass	TRUE	FALSE	FALSE	11.77	2.18	SEC7 homolog; TIC	2q13	
38119_at	GYPC	X12496	6	Pass	56.33	19.66	13	Pass	TRUE	FALSE	FALSE	25.85	2.18	glycophorin C (Gerbich blood group); GYPC	2q14-q21	
39594_f_at	MT1H	R93527	6	Pass	28.67	10.27	13	Pass	TRUE	FALSE	FALSE	13.15	2.18	metallothionein 1H; KIAA0909 protein; KIAA0909	16q13	
41421_at	KIAA0909	AB020716	6	Pass	12.17	5.12	12	Pass	TRUE	FALSE	FALSE	5.58	2.18	KIAA0909 protein; KIAA0909		
40712_at	ADAM8	D26579	6	Pass	44.00	15.09	13	Pass	TRUE	FALSE	FALSE	20.23	2.17	a disintegrin and metalloprotease domain 8; ADAM8	10q26.3	
40569_at	ZNF42	M58297	6	Pass	8.33	1.51	12	Pass	TRUE	FALSE	FALSE	3.83	2.17	zinc finger protein 42 (myeloid-specific retinoic acid-responsive); ZNF42	19q13.2-q13.4	
283_at	UQCRC1	L16842	6	Pass	27.17	10.46	12	Pass	TRUE	FALSE	FALSE	12.50	2.17	ubiquinol-cytochrome c reductase core protein 1; UQCRC1	3p21.3	
40100_at	LFP40	U72206	6	Pass	16.00	5.66	11	Pass	TRUE	FALSE	FALSE	7.36	2.17	thoracic guanine nucleotide exchange factor (GEF) 2; ARID2		
1878_g_at	ERCC1	M13194	6	Pass	14.33	4.50	10	Pass	TRUE	FALSE	FALSE	6.60	2.17	excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence); ERCC1	19q13.2-q13.3	
37329_at	NDUFB1	AF053070	6	Pass	17.00	6.07	12	Pass	TRUE	FALSE	FALSE	7.83	2.17	NADH dehydrogenase (ubiquinone) flavoprotein 1 (51kD); NDUFB1	11q13	
41172_at	UNK_AW	AW024285	6	Pass	35.33	17.08	13	Pass	TRUE	FALSE	FALSE	16.31	2.17	polynucleotide (RNA) II (DNA directed)	19p13.3	
41332_at	POLR2E	D38251	6	Pass	19.50	7.34	7	Pass	TRUE	FALSE	FALSE	9.00	2.17	polypeptide E (25kD); POLR2E		
1061_at	IL10RA	U00672	6	Pass	31.00	7.77	13	Pass	TRUE	FALSE	FALSE	14.31	2.17	interleukin 10 receptor, alpha; IL10RA	11q23	
32529_at	P63	X69910	6	Pass	14.00	8.88	13	Pass	TRUE	FALSE	FALSE	6.46	2.17	transmembrane protein (63kD); endoplasmic reticulum/Golgi intermediate compartment; p63	12	
32681_at	SLC9A1	S68616	6	Pass	24.67	6.77	13	Pass	TRUE	FALSE	FALSE	11.38	2.17	solute carrier family 9 (sodium/hydrogen exchanger), isoform 1 (anaplastic, Na+/H+; amiloride sensitive); SLC9A1	1p36.1-p35	

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38354_at	CEBPB	X52560	6	Pass	74.00	37.56	13	Pass	TRUE	FALSE	34.15	2.17	CCAAT/enhancer binding protein (CEBP), beta; CEBPB	20q13.1	
38397_at	UNK_U09	U09196	6	Pass	19.33	5.24	13	Pass	TRUE	FALSE	8.92	2.17			
39339_at	KIAA0792	AB018335	6	Pass	20.83	5.19	13	Pass	TRUE	FALSE	9.62	2.17	KIAA0792 gene product, KIAA0792		
41084_at	UNK_AJ63	AI659108	6	Pass	12.50	3.62	13	Pass	TRUE	FALSE	5.77	2.17	suppressor of Ty (S cerevisiae) 5 homolog, SUP75H	19q13	
35826_at	SUP75H	AF040253	6	Pass	16.83	5.08	9	Pass	TRUE	FALSE	7.78	2.16			
34231_at	UNK_AFO	AF074606	6	Pass	17.50	6.86	11	Pass	TRUE	FALSE	8.09	2.16	histone acetyltransferase, HBOA	Xq21	
33261_at	HLA-DRB	M16941	6	Pass	146.83	54.47	13	Pass	TRUE	FALSE	67.92	2.16	major histocompatibility complex, class II, DR beta	6p21.3	
33213_g_at	RRBP1	AF006751	6	Pass	8.83	5.12	11	Pass	TRUE	FALSE	4.09	2.16	ribosome binding protein 1 (deg 180kD homolog); RRB1	20p12	
37148_at	LILRB3	AF025533	6	Pass	44.50	25.98	13	Pass	TRUE	FALSE	20.62	2.16	leukocyte immunoglobulin like receptor subfamily B (with TM and ITIM domains), member 3, LILRB3	19q13.4	
35336_at	KIAA0668	AL021707	6	Pass	105.00	25.46	13	Pass	TRUE	FALSE	48.77	2.15	CDC37 (cell division cycle 37, S cerevisiae, homolog), CDC37	19	
37706_at	GLG1	U28811	6	Pass	14.67	2.50	11	Pass	TRUE	FALSE	6.82	2.15	Golgi apparatus protein 1, GLG1	16q22-q23	
37650_at	UNK_U41	U41315	6	Pass	43.33	11.57	13	Pass	TRUE	FALSE	20.15	2.15	makom, ring finger protein 1, MKRN1	7q34	
33360_at	KIAA1004	AB023221	6	Pass	20.33	3.01	13	Pass	TRUE	FALSE	9.46	2.15	f-box and leucine-rich repeat protein 11, FBXL11		
36933_at	NDRG1	D87953	6	Pass	19.67	6.25	13	Pass	TRUE	FALSE	9.15	2.15	N-type downstream regulated, NDRG1	8	
33824_at	KRT8	X74929	6	Pass	24.17	8.61	12	Pass	TRUE	FALSE	11.25	2.15	CGI-39 protein, keratin 8, KRT8, LOC51079	12q13	
36634_at	BTG2	U72649	6	Pass	38.67	16.39	13	Pass	TRUE	FALSE	18.00	2.15	BTG family, member 2, BTG2	1q32	
38641_at	UNK_AJ1	AJ133115	6	Pass	15.83	4.75	8	Pass	TRUE	FALSE	7.38	2.15	IMP (inosine monophosphate) dehydrogenase 1, IMP	7q31.3-q32	
40695_at	IMPDH1	J05272	6	Pass	35.67	14.80	13	Pass	TRUE	FALSE	16.62	2.15	adaptor-related protein complex 2, sigma 1 subunit, AP2S1	19q13.2-q13.3	
39347_at	CLAPS2	X97074	6	Pass	50.67	17.93	13	Pass	TRUE	FALSE	23.62	2.15	target of myb1 (chicken) homologue, TOM1	22q13.1	
39134_at	TOM1	AJ006973	6	Pass	7.50	2.66	10	Pass	TRUE	FALSE	3.50	2.14	ATPase, H+ transporting, lysosomal (vacuolar proton pump), subunit 1	Xq28	
35770_at	ATP6S1	D16469	6	Pass	44.00	20.62	13	Pass	TRUE	FALSE	20.54	2.14	metallothionein 1E (functional), MT1E	16q13	
36130_f_at	MT1E	R92331	6	Pass	25.67	6.95	12	Pass	TRUE	FALSE	12.00	2.14	signal transducer and activator of transcription 5A, STAT5A	17q11.2	
506_s_at	STAT5A	U43185	6	Pass	23.83	4.88	13	Pass	TRUE	FALSE	11.15	2.14	zinc finger protein 144 (ZNF148), ZNF144	17	
32192_g_at	ZNF144	D13969	6	Pass	18.00	4.20	7	Pass	TRUE	FALSE	8.43	2.14	solute carrier family 25 (mitochondrial carrier, oxoglutarate carrier), member 11, SLC25A11	17p13.3	
32197_at	SLC25A11	AF070548	6	Pass	11.17	4.31	13	Pass	TRUE	FALSE	5.23	2.13			
40980_at	UNK_W26	W26477	6	Pass	11.17	2.93	13	Pass	TRUE	FALSE	5.23	2.13			

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32717_at	NEURL	AF029729	4	Pass	27.75	5.74	8	Pass	TRUE	FALSE	13.00	2.13	neutralized (Drosophila)-like; NEURL	10q25.1	
38700_at	CSRP1	M33146	6	Pass	11.83	3.66	11	Pass	TRUE	FALSE	5.55	2.13	cysteine and glycine-rich protein 1; CSRP1	1q32	
38718_at	DKFZP586A1050101		6	Pass	8.00	2.10	12	Pass	TRUE	FALSE	3.75	2.13	DKFZP586F1519 protein, DKFZP586E1519		
33390_at	UNK_AA203487		6	Pass	83.67	49.40	9	Pass	TRUE	FALSE	39.22	2.13	glutathione S-t anferase pi; GSTP1	11q13	
829_s_at	U21689		6	Pass	51.83	30.04	10	Pass	TRUE	FALSE	24.30	2.13	mannosyl (alpha-1,3)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase; MGAT1	5q35	
39778_at	MGAT1	M55621	6	Pass	39.67	12.47	13	Pass	TRUE	FALSE	18.62	2.13			
40153_at	ABCB2	X57522	6	Pass	29.50	8.67	13	Pass	TRUE	FALSE	13.85	2.13	ATP-binding cassette, subfamily B (MDR/TAP), member 2; ABCB2	6p21.3	
404_at	IL4R	X52425	6	Pass	29.00	8.29	13	Pass	TRUE	FALSE	13.62	2.13	interleukin 4 receptor, IL4R	16p11.2-12.1	
37101_at	DKFZP564A1050008		6	Pass	19.17	5.19	12	Pass	TRUE	FALSE	9.00	2.13	DKFZP564A063 protein, DKFZP564A063		
32904_at	PRF1	M28393	6	Pass	86.00	65.71	13	Pass	TRUE	FALSE	40.38	2.13	perform 1 (performing protein); PRF1	10q22	
33228_g_at	IL10RB	A1984234	6	Pass	55.50	17.95	13	Pass	TRUE	FALSE	26.08	2.13	interleukin 10 receptor, beta; IL10RB	21q22.11	
40421_at	PIN1	U49070	6	Pass	8.67	2.58	12	Pass	TRUE	FALSE	4.08	2.12	protein (pepducyl-prolyl cis/trans isomerase) NIMA interacting 1; PIN1	19p13	
691_g_at	P4H1B	J02783	6	Pass	49.17	17.06	12	Pass	TRUE	FALSE	23.17	2.12	procollagen-proline, 2-oxoglutarate 4-hydroxylase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase, thyroid hormone binding tumor necrosis factor receptor superfamily, member 1A; TNFRSF1A specific); TUBA1	17q25	
1563_s_at	TNFRSF1A	M58286	6	Pass	28.17	11.91	11	Pass	TRUE	FALSE	13.27	2.12	zinc finger protein 266, ZNF266	12p13.2	
330_s_at	TUBA1	X06956	6	Pass	39.17	9.47	13	Pass	TRUE	FALSE	18.46	2.12	H2A histone family, member O; H2AFO	2q	
41622_r_at	ZNF266	AA868898	6	Pass	6.83	1.83	9	Pass	TRUE	FALSE	3.22	2.12	peroxisome biogenesis factor 10; PEX10		
286_at	H2AFO	L19779	6	Pass	61.50	25.26	13	Pass	TRUE	FALSE	29.00	2.12	interferon induced transmembrane protein 3 (L8U); IFITM3		
41282_s_at	PEX10	AA194159	4	Pass	11.50	3.70	7	Pass	TRUE	FALSE	5.43	2.12	E74-like factor 4 (cis domain transcription factor); ELF4	Xq26	
41745_at	IFITM3	X57352	6	Pass	207.17	120.90	13	Pass	TRUE	FALSE	97.85	2.12	CD19 antigen, CD19 linker for activation of T cells; LAT	16p11.2	
31845_at	ELF4	U32645	6	Pass	18.17	7.70	12	Pass	TRUE	FALSE	8.58	2.12	ubiquitin specific protease 11; USP11		
1116_at	CD19	M28170	6	Pass	6.83	1.33	13	Pass	TRUE	FALSE	3.23	2.12	docking protein 2, 50kD, DOK2		
40685_at	LAT	AJ223280	6	Pass	27.67	4.37	12	Pass	TRUE	FALSE	13.08	2.11	biliverdin reductase B (flavin reductase (NADPH)), BLVRR	19q13.1-13.2	
162_at	USP11	U44839	6	Pass	46.17	9.66	13	Pass	TRUE	FALSE	21.85	2.11	ubiquitin specific protease 4 (proto-oncogene), USP4	3p21.3	
34906_g_at	UNK_AA977136		6	Pass	32.50	8.85	13	Pass	TRUE	FALSE	15.38	2.11			
31514_at	DOK2	AF034970	6	Pass	25.33	8.80	10	Pass	TRUE	FALSE	12.00	2.11			
37002_at	BLVRR	D32143	6	Pass	25.00	11.47	13	Pass	TRUE	FALSE	11.85	2.11			
1357_at	USP4	U20657	6	Pass	12.33	4.59	13	Pass	TRUE	FALSE	5.85	2.11			



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32317_s_at	SULT1A2	U34804	6	Pass	24.50	11.33	13	Pass	TRUE	FALSE	11.62	2.11	sulfotransferase family 1A, phenol-preferring, member 6p12.1-2.sulfotransferase family 1A, phenol-preferring, member 1,	16p12.1, 1-2
35774_r_at	NDUFB7	AA527880	6	Pass	24.33	7.55	13	Pass	TRUE	FALSE	11.54	2.11	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7 (18kD, B18), NDUFB7	10q25
40870_g_at	RBM6	AF069517	6	Pass	12.17	3.97	13	Pass	TRUE	FALSE	5.77	2.11	RNA binding motif protein 6, RBM6	3p21.3
39081_at	MT2A	A1547258	6	Pass	11.83	4.31	13	Pass	TRUE	FALSE	5.62	2.11	metallothionein 2A,	16q13
1375_s_at	TIMP2	M32304	4	Pass	14.75	8.26	9	Pass	TRUE	FALSE	7.00	2.11	tissue inhibitor of metalloproteinase 2, TIMP2	17q25
36615_at	ARP	M83751	4	Pass	19.75	5.50	8	Pass	TRUE	FALSE	9.38	2.11	Arginine-rich protein, minichromosome maintenance deficient (S cerevisiae) 2 (mitotin) MCM2	3p21.1
35512_at	MCM2	D21063	6	Pass	17.50	3.62	13	Pass	TRUE	FALSE	8.31	2.11	minichromosome maintenance deficient (S cerevisiae) 2 (mitotin) MCM2	3q21
37801_at	Tf6	AF112972	6	Pass	9.00	3.58	11	Pass	TRUE	FALSE	4.27	2.11	Tf6 protein, Tf6	6p21.3
38021_at	UNK_AJ0	AJ012008	6	Pass	10.00	2.45	12	Pass	TRUE	FALSE	4.75	2.11	dimethylarginine dimethylaminohydrolase 2, DDH2	6p21.3
37939_at	UNK_AL0	AL022318	6	Pass	45.67	11.69	13	Pass	TRUE	FALSE	21.69	2.11	small inducible cytokine A5 (RANTES), SCYA5	17q11.2-q12
1405_l_at	SCYA5	M21121	6	Pass	68.17	25.93	13	Pass	TRUE	FALSE	32.38	2.10	small inducible cytokine A5 (RANTES), SCYA5	17q11.2-q12
35150_at	TNFRSF5	X60592	6	Pass	28.33	7.66	13	Pass	TRUE	FALSE	13.46	2.10	tumor necrosis factor receptor superfamily, member 5, TNFRSF5	20q12-q13.2
34864_at	CGI-57	AF070638	6	Pass	38.17	12.35	13	Pass	TRUE	FALSE	18.15	2.10	hypothetical protein, CGI-57	
34861_at	GOLGA3	D63997	6	Pass	10.83	1.47	13	Pass	TRUE	FALSE	5.15	2.10	golgi autoantigen, golgi subfamily a, 3, GOLGA3	12
32253_at	ATN1L	AB007927	6	Pass	31.67	4.97	13	Pass	TRUE	FALSE	15.08	2.10	arginine glutamic acid dipeptide RE repeats, RERE	1p36.1-p36.2
41264_at	UNK_AL0	AL050172	4	Pass	6.00	2.94	7	Pass	TRUE	FALSE	2.86	2.10	ubiquitin specific protease 15, USP15	12q14
34295_at	USP15	AB011101	6	Pass	6.00	3.16	7	Pass	TRUE	FALSE	2.86	2.10	ubiquitin specific protease 15, USP15	12q14
40780_at	CTBP2	AF016507	6	Pass	15.33	10.46	13	Pass	TRUE	FALSE	7.31	2.10	C-terminal binding protein 2, CTBP2	21q21.3
38453_at	ICAM2	X15606	6	Pass	25.50	5.36	13	Pass	TRUE	FALSE	12.15	2.10	intercellular adhesion molecule 2, ICAM2	17q23-q25
36889_at	FCER1G	M33195	6	Pass	56.00	35.60	13	Pass	TRUE	FALSE	26.69	2.10	Fc fragment of IgE, high affinity I, receptor for, gamma polypeptide, FCER1G	1q23
38053_s_at	BRE	AF015767	6	Pass	9.83	3.13	13	Pass	TRUE	FALSE	4.69	2.10	brain and reproductive organ-expressed (TNFRSF1A modulator), BRE	
32816_at	SGT	AL050156	6	Pass	6.67	2.25	11	Pass	TRUE	FALSE	3.18	2.10	small glutamine-rich tetrapeptide repeat (TPR)-containing, SGT	19p13
36986_at	UNK_AL0	AL031295	6	Pass	117.17	29.18	13	Pass	TRUE	FALSE	55.92	2.10	cryptopharynx RNA synthetase, WARS	14q23-q31
38121_at	WARS	X59892	6	Pass	34.17	22.83	13	Pass	TRUE	FALSE	16.31	2.10	cryptopharynx RNA synthetase, WARS	14q23-q31
32877_l_at	UNK_AA5	AA524802	4	Pass	49.50	23.69	11	Pass	TRUE	FALSE	23.64	2.09	Trachea Collins-Franceschetti syndrome 1, q33.1	5q32-q33.1
40596_at	TCOF1	U76366	6	Pass	22.33	4.55	12	Pass	TRUE	FALSE	10.67	2.09	Trachea Collins-Franceschetti syndrome 1, TCOF1	5q32-q33.1

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39072_at	MXI1	L07648	6	Pass	28.50	13.14	13	Pass	TRUE	FALSE	FALSE	13.62	MAX-interacting protein 1; MXI1	10q24- q25	
37033_s_at	GPX1	X13710	6	Pass	279.17	52.77	13	Pass	TRUE	FALSE	FALSE	133.38	glutathione peroxidase 1, GPX1	3p21.3	
32195_at	UNK_AL0	AL049450	6	Pass	14.17	5.12	13	Pass	TRUE	FALSE	FALSE	6.77	KIAA0224 gene product,	16	
37390_at	KIAA0224	D86977	6	Pass	13.67	2.94	13	Pass	TRUE	FALSE	FALSE	6.54	KIAA0224		
38449_at	UNK_W28	W28931	6	Pass	15.67	8.94	8	Pass	TRUE	FALSE	FALSE	7.50	cuker yotic translation initiation factor 3, subunit 3 (gamma, 40kD), EIF3S3		
36187_at	RNH	X13973	6	Pass	39.50	15.10	13	Pass	TRUE	FALSE	FALSE	18.92	ribonuclease/angiogenin inhibitor, RNH	11p15.5	
34408_at	RTN2	AF004222	6	Pass	12.00	3.35	8	Pass	TRUE	FALSE	FALSE	5.75	reticulon 2, RTN2		
36798_g_at	SPN	J04168	6	Pass	47.50	14.95	13	Pass	TRUE	FALSE	FALSE	22.77	sirophorn (gp115, leukosialin, CD43), SPN	16p11.2	
38412_at	PPP1R11	U53588	6	Pass	17.00	4.24	13	Pass	TRUE	FALSE	FALSE	8.15	protein phosphatase 1, regulatory (inhibitor) subunit 11; PPP1R11	6p21.3	
34033_s_at	LILRA2	AF025531	6	Pass	33.67	18.47	13	Pass	TRUE	FALSE	FALSE	16.15	leukocyte immunoglobulin like receptor subfamily A (with TM domain), member 2; LILRA2	19q13.4	
241_g_at	SRM	M64231	6	Pass	16.67	3.88	12	Pass	TRUE	FALSE	FALSE	8.00	spermidine synthase, SRM	1p36-p22	
41316_s_at	SAFB	U72355	6	Pass	20.67	5.05	13	Pass	TRUE	FALSE	FALSE	9.92	scaffold attachment factor B, SAFB	19p13	
36591_at	TUBA1	X06956	6	Pass	114.67	24.81	13	Pass	TRUE	FALSE	FALSE	55.08	tubulin, alpha 1 (tests specific), TUBA1	2q	
38830_at	ABCF3	U66685	5	Pass	9.20	3.77	7	Pass	TRUE	FALSE	FALSE	4.43	ATP-binding cassette, sub- family 1 (GCN20), member 3, hypothetical protein FLJ11198	3q25.1- q25.2	
38841_at	GDBR1	AF068195	6	Pass	9.00	4.52	12	Pass	TRUE	FALSE	FALSE	4.33	ABCF3, FLJ11198 putative glioblastoma cell differentiation- related, putative glioblastoma cell differentiation-related protein, GDBR1, GDBR1	9	
37641_at	MTAP44	D28915	6	Pass	11.50	7.48	13	Pass	TRUE	FALSE	FALSE	5.54	meritonin-induced, hepatitis C-associated microtubular aggregat- in (44kD); MTAP44	1	
41838_at	UNK_X99	X99270	6	Pass	7.50	2.35	13	Pass	TRUE	FALSE	FALSE	3.62	contig. ORF, HSXQ28ORF		
41614_at	KIAA0708	AB014608	6	Pass	6.83	2.04	10	Pass	TRUE	FALSE	FALSE	3.30	KIAA0708 protein, KIAA0708		
448_s_at	MEN1	U93257	6	Pass	6.83	1.83	10	Pass	TRUE	FALSE	FALSE	3.30	multiple endocrine neoplasia 1, MEN1	11q13	
32140_at	SORL1	Y08110	6	Pass	81.00	22.91	13	Pass	TRUE	FALSE	FALSE	39.15	sortilin-related receptor, L (DLR class) A repeats- containing, SORL1	11q23.2- q24.2	
32592_at	KIAA0323	AB002321	6	Pass	17.17	4.67	13	Pass	TRUE	FALSE	FALSE	8.31	KIAA0323 protein, KIAA0323		
36709_at	ITGAX	Y00093	6	Pass	30.83	17.06	13	Pass	TRUE	FALSE	FALSE	14.92	integrin, alpha X (antigen CD11C (p150), alpha polypeptide), ITGAX	16p11.2	
41387_r_at	KIAA0346	AB002344	6	Pass	11.50	6.16	7	Pass	TRUE	FALSE	FALSE	5.57	KIAA0346 protein, KIAA0346	17p13.1	
41625_at	TRAP240	AB011165	6	Pass	5.83	3.19	12	Pass	TRUE	FALSE	FALSE	2.83	thyroid hormone receptor- associated protein, 240 kDa subunit, TRAP240	17	
35254_at	FLN29	AB007447	6	Pass	15.67	4.63	13	Pass	TRUE	FALSE	FALSE	7.62	FLN29 gene product, FLN29	12q	

Affy Qualifier	Affy Name	accession	sum of Present Calls	4 of 6 present	Avg Freq RA	Std Dev RA	sum of abs dec	7 of 13 present	Present in RA and Normal	Present in RA, Absent in Normal	Avg Freq (Normal)	Fold Change	Name	Chromosome	Phosphatase
38780_at	AKR1A1	J04794	6	Pass	28.00	8.65	13	Pass	TRUE	FALSE	13.62	2.06	aldo-keto reductase family 1, member A1 (aldehyde reductase); AKR1A1	1p33-p32	
40890_at	MTX1	U46920	6	Pass	27.83	7.55	13	Pass	TRUE	FALSE	13.54	2.06	metaxin 1; MTX1	1q21	
39412_at	ZNF173	U09825	6	Pass	12.33	5.57	9	Pass	TRUE	FALSE	6.00	2.06	zinc finger protein 173; ZNF173	6p21.3	
33215_g_at	RPMS12	Y11681	6	Pass	33.67	6.53	13	Pass	TRUE	FALSE	16.38	2.05	ribosomal protein, mitochondrial, S12; RPMS12	19q13.1	
34310_at	APRT	Y00486	5	Pass	25.40	6.27	11	Pass	TRUE	FALSE	12.36	2.05	adenine phosphoribosyltransferase; APRT	16q24	
33409_at	FKBP2	AA158243	6	Pass	15.00	4.65	13	Pass	TRUE	FALSE	7.31	2.05	FK-506-binding protein 2 (13kD); FKBP2	11q13.1-q13.3	
33748_at	KIAA0223	D86976	6	Pass	53.50	13.14	13	Pass	TRUE	FALSE	26.08	2.05	minor histocompatibility antigen H1A-1; KIAA0223	19p13.3	
33323_r_at	SFN	X57348	6	Pass	11.50	4.72	13	Pass	TRUE	FALSE	5.62	2.05	stratifin; SFN	1p	
32228_at	ADTAB	AB020706	5	Pass	19.60	6.77	7	Pass	TRUE	FALSE	9.57	2.05	adaptor-related protein complex 2, alpha 2	11	
32236_at	UBE2G2	AF032456	6	Pass	25.17	11.18	13	Pass	TRUE	FALSE	12.31	2.04	ubiquitin-conjugating enzyme E2G 2 (homologous to yeast UBC7); UBE2G2	21q22.3	
32629_f_at	BTN3A1	U90552	6	Pass	111.33	28.98	13	Pass	TRUE	FALSE	54.46	2.04	butyrophilin, subfamily 3, member A1; BTN3A1	6p22.1	
35769_at	GPR56	A1011001	6	Pass	23.17	9.30	12	Pass	TRUE	FALSE	11.33	2.04	G protein-coupled receptor 56; GPR56	16q13	
39541_at	UNK_W52	W52003	4	Pass	12.00	4.08	8	Pass	TRUE	FALSE	5.88	2.04	microspherule protein 1; MCRS1	12	
33898_at	MCRS1	AF015508	6	Pass	16.33	5.28	8	Pass	TRUE	FALSE	8.00	2.04	KIAA0275 gene product; KIAA0275	10	
36155_at	KIAA0275	D87465	6	Pass	67.83	11.11	13	Pass	TRUE	FALSE	33.23	2.04	tubulin, beta polypeptide; TUBB	6p21.3	
709_at	UNK_J003	J00314	6	Pass	16.50	3.62	11	Pass	TRUE	FALSE	8.09	2.04	stem cell growth factor, lymphocyte secreted C-type lectin; SCGF	19q13.3	
37147_at	SCGF	AF020044	6	Pass	18.33	5.85	12	Pass	TRUE	FALSE	9.00	2.04	RNA binding motif protein 6; RBM6	3p21.3	
39865_at	UNK_A189	A1890903	6	Pass	9.67	2.66	12	Pass	TRUE	FALSE	4.75	2.04	CD81 antigen (target of antiproliferative antibody 1); CD81	11p15	
40869_at	RBM6	AF069517	6	Pass	9.67	2.73	12	Pass	TRUE	FALSE	4.75	2.04	ATP-binding cassette, subfamily F (GCN20), member 1; ABCF1	6p21.33	
35282_r_at	CD81	M33680	6	Pass	77.33	22.92	13	Pass	TRUE	FALSE	38.00	2.04	gamma-glutamyltransferase 1; gamma-glutamyltransferase 2	22q11.1-q11.2,22q11.23	
39141_at	ABCF1	AF027302	6	Pass	12.83	4.17	13	Pass	TRUE	FALSE	6.31	2.03	signal transducer and activator of transcription 1; STAT1	2q32.2	
715_s_at	GGT1	D87002	6	Pass	7.67	2.07	13	Pass	TRUE	FALSE	3.77	2.03	NADH dehydrogenase (ubiquinone) Fe-S protein 8 (23kD) (NADH-coenzyme Q reductase); NDUFS8	11q13	
33338_at	STAT1	M97936	6	Pass	20.00	9.80	12	Pass	TRUE	FALSE	9.83	2.03	MYC-associated zinc finger protein (purine-binding transcription factor); MYC	16p11.2	
38257_at	NDUFS8	AF038406	6	Pass	10.17	5.56	10	Pass	TRUE	FALSE	5.00	2.03	small inducible cytokine A5 (RANTES); SCYA5	17q11.2-q12	
32553_at	MAZ	M94046	6	Pass	96.33	20.40	13	Pass	TRUE	FALSE	47.38	2.03			
1404_r_at	SCYA5	M21121	6	Pass	10.50	3.94	12	Pass	TRUE	FALSE	5.17	2.03			
37256_at	UNK_A182	A1829890	6	Pass	10.83	2.86	12	Pass	TRUE	FALSE	5.33	2.03			

Affy Qualifier	Affy Name	accession	sum of Present Calls	4 of 6 present	Avg Freq RA	Std Dev RA	sum of abs dec	7 of 13 present	Present in RA and Normal	Present in RA, Absent in Normal	Absent in RA, Present in Normal	Avg Freq (Normal)	Fold Change RA / Normal	Name	Chromosome	Aliases or Phosphatase
40994_at	DEDD	AF043733	6	Pass	21.67	9.05	12	Pass	TRUE	FALSE	FALSE	10.67	2.03	death effector domain-containing; DEDD		
38864_at	UNK_W26	W26851	6	Pass	13.00	2.00	10	Pass	TRUE	FALSE	FALSE	6.40	2.03			
41267_at	KIAA1049	AB028972	6	Pass	22.33	6.95	13	Pass	TRUE	FALSE	FALSE	11.00	2.03	KIAA1049 protein,	16	
32080_at	TETRA	L11669	6	Pass	42.17	12.22	13	Pass	TRUE	FALSE	FALSE	20.77	2.03	tetracycline transporter-like protein, TETRA	4p16.3	*
35944_at	UNK_AL0	AL031228	5	Pass	14.20	5.54	7	Pass	TRUE	FALSE	FALSE	7.00	2.03	Cluster Incl AL031228, Human DNA sequence from clone 1033B10 on chromosome 6p21.2-21.31. Contains the BING5 gene, exons 11 to 15 of the BING4 gene, the gene for GalT3 (beta3-Galactosyltransferase), the RPS18 (40S ribosomal protein S18) gene, the SACM2L (suppressor of actin mutation 2, yeast, homolog) gene, a pseudogene similar to IA1-SP1, a Pseudogene similar to zinc finger genes, the RING1 gene, the gene for HKE6 (RING2), the gene for HKE4 (RING5), the RXRB (Retinoid X receptor beta) gene, the COL11A2 (collagen, type XI, alpha 2) gene, the H1A-DPB2 pseudogene and part of the HLA-DPA3 pseudogene	6p21.3	*
33388_at	UNK_AL0	AL080223	6	Pass	22.00	5.40	13	Pass	TRUE	FALSE	FALSE	10.85	2.03	Contains predicted CpG		
40787_at	UNK_U90	U90911	6	Pass	12.17	3.66	13	Pass	TRUE	FALSE	FALSE	6.00	2.03			
35911_r_at	MMPL1	AJ003147	6	Pass	24.50	8.14	12	Pass	TRUE	FALSE	FALSE	12.08	2.03	matrix metalloproteinase-like 1, MMPL1	16p13.3	
37003_at	CD63	X62654	6	Pass	29.00	14.71	13	Pass	TRUE	FALSE	FALSE	14.31	2.03	CD63 antigen (melanoma antigen), CD63	12q12-q13	*
38475_at	DCTN-50	U50733	6	Pass	14.50	5.54	13	Pass	TRUE	FALSE	FALSE	7.15	2.03	dynamitin (dynactin complex, 50 kD subunit), DCTN-50	12	
870_f_at	MT3	M93311	6	Pass	31.50	13.44	11	Pass	TRUE	FALSE	FALSE	15.55	2.03	metallothionein 3 (growth inhibitory factor (neurotrophic)), MT3	16q13	
34178_at	UNK_A188	A1884738	6	Pass	7.17	1.60	13	Pass	TRUE	FALSE	FALSE	3.54	2.03	zinc finger protein 297, ZNF297	6p21.3	
36167_at	ATP6F	D89052	6	Pass	64.50	29.51	13	Pass	TRUE	FALSE	FALSE	31.85	2.03	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 21kD, syntaxin 4A (placental), STX4A	1p32.3	*
37911_at	STX4A	U07158	6	Pass	13.33	3.88	12	Pass	TRUE	FALSE	FALSE	6.58	2.03			
38523_f_at	U2AF1RS2	D49677	6	Pass	13.67	2.58	12	Pass	TRUE	FALSE	FALSE	6.75	2.02	U2 small nuclear ribonucleoprotein auxiliary factor, small subunit 2, U2AF1RS2	Xp22.1	
37931_at	CENPB	X05299	6	Pass	10.67	2.42	11	Pass	TRUE	FALSE	FALSE	5.27	2.02	centomere protein B (80kD), CENPB	20p13	
35124_at	ALOX12	M62982	6	Pass	14.00	4.69	13	Pass	TRUE	FALSE	FALSE	6.92	2.02	arachidonate 12-lipoxygenase, ALOX12	17p13.1	

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32523_at	CLTB	M20470	6	Pass	5.17	1.83	9	Pass	FALSE	2.56	2.02	clathrin, light polypeptide (Leb); CLTB	4q2-q3	
37442_at	UNK_AL0	AL050378	6	Pass	18.00	6.32	13	Pass	FALSE	8.92	2.02	oxoglutarate	7p14-p13	
40470_at	OGDH	D10523	5	Pass	14.40	3.85	7	Pass	FALSE	7.14	2.02	dehydrogenase	1p34	
37759_at	LAPTM5	U51240	6	Pass	229.50	56.06	13	Pass	FALSE	113.85	2.02	Lysosomal-associated multi-spanning membrane protein-5; LAPTM5	11p15.5	
37126_at	SSA1	M62800	5	Pass	15.00	5.83	9	Pass	FALSE	7.44	2.01	Sjogren syndrome antigen A1 (SSKD, ribonucleoprotein autoantigen SS-A/Ro); SSA1	16	
34260_at	KIAA0683	AB014583	5	Pass	6.80	2.49	8	Pass	FALSE	3.38	2.01	KIAA0683 gene product; KIAA0683	16	
1468_at	TRAP1	U12595	6	Pass	11.00	2.10	13	Pass	FALSE	5.46	2.01	heat shock protein 75; TRAP1	1q41-q43	kinase
37272_at	ITPKB	X57206	6	Pass	28.50	6.38	13	Pass	FALSE	14.15	2.01	inositol 1,4,5-trisphosphate 3-kinase B	19q13.1	
1830_s_at	TGFB1	M38449	6	Pass	30.67	6.80	13	Pass	FALSE	15.23	2.01	transforming growth factor, beta 1; TGFB1	6p21.3	
35685_at	RING1	Z14000	6	Pass	15.33	3.93	13	Pass	FALSE	7.62	2.01	ring finger protein 1; RING1	11q13	
1295_at	RELA	L19067	6	Pass	39.17	15.38	13	Pass	FALSE	19.46	2.01	v-rel avian reticuloendotheliosis viral oncogene homolog A (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (n65)); RELA	11q13	
32271_at	FOSL1	X16707	4	Pass	9.25	2.75	10	Pass	FALSE	4.60	2.01	FOS-like antigen-1; aquaporin 9; AQP9	7p14-p12	
34435_at	AQP9	AB008775	6	Pass	7.83	5.19	10	Pass	FALSE	3.90	2.01	acyloxyacyl hydrolase (neutrophil); AOA9		
37647_at	AOAH	M62840	6	Pass	25.00	14.34	13	Pass	FALSE	12.46	2.01	prostatic binding protein; PBP		
32611_at	PBP	X75252	6	Pass	14.50	5.09	13	Pass	FALSE	7.23	2.01	MYC promoter-binding protein 1; enolase 1; (ahh); ENO1; MPB1	1p36.3-p36.2, 1p35	
2035_s_at	MPB1	M55914	6	Pass	125.67	55.44	13	Pass	FALSE	62.69	2.00	capping protein (actin filament) muscle Z-line, beta; CAPZB	1p36.1	
37012_at	CAPZB	U03271	6	Pass	65.83	19.11	13	Pass	FALSE	32.85	2.00	MAP-kinase activating death domain; MADD	11p11.2	
34830_at	UNK_W25	W25986	6	Pass	36.83	7.31	13	Pass	FALSE	18.38	2.00	KIAA0140 gene product; KIAA0140		
38398_at	MADD	AB002356	6	Pass	16.33	6.09	13	Pass	FALSE	9.15	2.00	DKFZP586B0519 protein; DKFZP586B0519	8q24	
40143_at	KIAA0140	D50930	6	Pass	18.33	7.23	13	Pass	FALSE	16.23	2.00	Src-like adapter, SLA	17q11.2	
35205_at	DKFZP586	AL050280	6	Pass	32.50	9.40	13	Pass	FALSE	11.15	2.00	tetratricopeptide repeat domain 2; TTC2	1q21.1	
1427_g_at	SLA	D89077	6	Pass	22.33	10.86	13	Pass	FALSE	11.15	2.00	papillary renal cell carcinoma (translocation-associated); PRC		
41800_s_at	TTC2	U46571	6	Pass	22.33	5.65	13	Pass	FALSE	5.00	2.00	solute carrier family 1 (neutral amino acid transporter), member 5; SLC1A5	19q13.3	
39149_at	PRCC	X99720	6	Pass	10.00	2.00	7	Pass	FALSE	4.00	2.00	SI2-B homolog; DKFZP547G1110		
41778_at	SLC1A5	U53347	5	Pass	8.00	3.61	8	Pass	FALSE	3.50	2.00			
40149_at	DKFZP547	AL049924	6	Pass	7.00	0.63	8	Pass	FALSE					

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453_at	SMARCC2	U66616	6	Pass	5.00	2.00	8	Pass	TRUE	FALSE	2.50	2.00	SWI/SNF related, matrix associated, actin dependent	12q13-q23	
40840_at	PPIF	M80254	6	Pass	8.67	2.66	9	Pass	TRUE	FALSE	4.33	2.00	peptidylprolyl isomerase F (cyclophilin F), PPIF	10q22-q25	
1014_at	POLG	U60325	6	Pass	10.00	3.41	12	Pass	TRUE	FALSE	5.00	2.00	polynuclease (DNA directed), gamma, POLG	15q25	
1243_at	DDB2	U18300	6	Pass	11.00	1.79	12	Pass	TRUE	FALSE	5.50	2.00	damage-specific DNA binding protein 2 (48kD); DDB2	11p12-p11	
1487_at	ESRRA	L38487	6	Pass	12.00	5.18	12	Pass	TRUE	FALSE	6.00	2.00	estrogen-related receptor alpha, ESRRA	11q12	
197_at	NME3	U29656	6	Pass	10.50	2.88	12	Pass	TRUE	FALSE	5.25	2.00	non-metastatic cells 1, protein expressed in, NME3	16q13	
32533_s_at	VAMP5	AF054825	6	Pass	9.50	4.23	12	Pass	TRUE	FALSE	4.75	2.00	vesicle-associated membrane protein 5 (involved in, VAMP5)		
34871_at	UNK_W30	W30677	6	Pass	18.67	6.83	12	Pass	TRUE	FALSE	9.33	2.00			
36815_at	UNK_AF0	AF038185	6	Pass	16.00	3.41	12	Pass	TRUE	FALSE	8.00	2.00			
40282_s_at	DF	M84526	6	Pass	38.00	25.78	13	Pass	TRUE	FALSE	19.00	2.00	D component of complement (adipsin), DF	19	
36645_at	RELA	L19067	6	Pass	33.67	12.82	13	Pass	TRUE	FALSE	16.85	2.00	v-ei avian reticuloendotheliosis viral oncogene homolog A (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (n65D), RELA	11q13	
41471_at	S100A9	W72424	6	Pass	313.50	166.70	13	Pass	TRUE	FALSE	157.00	2.00	S100 calcium-binding protein A9 (calgranulin B), S100A9	1q21	
33227_at	IL10RB	A1984234	6	Pass	15.33	6.22	13	Pass	TRUE	FALSE	7.69	1.99	interleukin 10 receptor, beta, IL10RB	21q22.11	
38308_g_at	KIAA0607	AB011179	6	Pass	30.50	9.31	13	Pass	TRUE	FALSE	15.31	1.99	neurochondin, KIAA0607	1	
36145_at	SIAHBP1	U51586	6	Pass	22.50	6.77	13	Pass	TRUE	FALSE	11.31	1.99	siah binding protein 1, siah binding protein 1, FBP interacting repressor, p19, p21, p22, p23, p24, p25, p26, p27, p28, p29, p30, p31, p32, p33, p34, p35, p36, p37, p38, p39, p40, p41, p42, p43, p44, p45, p46, p47, p48, p49, p50, p51, p52, p53, p54, p55, p56, p57, p58, p59, p60, p61, p62, p63, p64, p65, p66, p67, p68, p69, p70, p71, p72, p73, p74, p75, p76, p77, p78, p79, p80, p81, p82, p83, p84, p85, p86, p87, p88, p89, p90, p91, p92, p93, p94, p95, p96, p97, p98, p99, p100, p101, p102, p103, p104, p105, p106, p107, p108, p109, p110, p111, p112, p113, p114, p115, p116, p117, p118, p119, p120, p121, p122, p123, p124, p125, p126, p127, p128, p129, p130, p131, p132, p133, p134, p135, p136, p137, p138, p139, p140, p141, p142, p143, p144, p145, p146, p147, p148, p149, p150, p151, p152, p153, p154, p155, p156, p157, p158, p159, p160, p161, p162, p163, p164, p165, p166, p167, p168, p169, p170, p171, p172, p173, p174, p175, p176, p177, p178, p179, p180, p181, p182, p183, p184, p185, p186, p187, p188, p189, p190, p191, p192, p193, p194, p195, p196, p197, p198, p199, p200, p201, p202, p203, p204, p205, p206, p207, p208, p209, p210, p211, p212, p213, p214, p215, p216, p217, p218, p219, p220, p221, p222, p223, p224, p225, p226, p227, p228, p229, p230, p231, p232, p233, p234, p235, p236, p237, p238, p239, p240, p241, p242, p243, p244, p245, p246, p247, p248, p249, p250, p251, p252, p253, p254, p255, p256, p257, p258, p259, p260, p261, p262, p263, p264, p265, p266, p267, p268, p269, p270, p271, p272, p273, p274, p275, p276, p277, p278, p279, p280, p281, p282, p283, p284, p285, p286, p287, p288, p289, p290, p291, p292, p293, p294, p295, p296, p297, p298, p299, p300, p301, p302, p303, p304, p305, p306, p307, p308, p309, p310, p311, p312, p313, p314, p315, p316, p317, p318, p319, p320, p321, p322, p323, p324, p325, p326, p327, p328, p329, p330, p331, p332, p333, p334, p335, p336, p337, p338, p339, p340, p341, p342, p343, p344, p345, p346, p347, p348, p349, p350, p351, p352, p353, p354, p355, p356, p357, p358, p359, p360, p361, p362, p363, p364, p365, p366, p367, p368, p369, p370, p371, p372, p373, p374, p375, p376, p377, p378, p379, p380, p381, p382, p383, p384, p385, p386, p387, p388, p389, p390, p391, p392, p393, p394, p395, p396, p397, p398, p399, p400, p401, p402, p403, p404, p405, p406, p407, p408, p409, p410, p411, p412, p413, p414, p415, p416, p417, p418, p419, p420, p421, p422, p423, p424, p425, p426, p427, p428, p429, p430, p431, p432, p433, p434, p435, p436, p437, p438, p439, p440, p441, p442, p443, p444, p445, p446, p447, p448, p449, p450, p451, p452, p453, p454, p455, p456, p457, p458, p459, p460, p461, p462, p463, p464, p465, p466, p467, p468, p469, p470, p471, p472, p473, p474, p475, p476, p477, p478, p479, p480, p481, p482, p483, p484, p485, p486, p487, p488, p489, p490, p491, p492, p493, p494, p495, p496, p497, p498, p499, p500, p501, p502, p503, p504, p505, p506, 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p673, p674, p675, p676, p677, p678, p679, p680, p681, p682, p683, p684, p685, p686, p687, p688, p689, p690, p691, p692, p693, p694, p695, p696, p697, p698, p699, p700, p701, p702, p703, p704, p705, p706, p707, p708, p709, p710, p711, p712, p713, p714, p715, p716, p717, p718, p719, p720, p721, p722, p723, p724, p725, p726, p727, p728, p729, p730, p731, p732, p733, p734, p735, p736, p737, p738, p739, p740, p741, p742, p743, p744, p745, p746, p747, p748, p749, p750, p751, p752, p753, p754, p755, p756, p757, p758, p759, p760, p761, p762, p763, p764, p765, p766, p767, p768, p769, p770, p771, p772, p773, p774, p775, p776, p777, p778, p779, p780, p781, p782, p783, p784, p785, p786, p787, p788, p789, p790, p791, p792, p793, p794, p795, p796, p797, p798, p799, p800, p801, p802, p803, p804, p805, p806, p807, p808, p809, p810, p811, p812, p813, p814, p815, p816, p817, p818, p819, p820, p821, p822, p823, p824, p825, p826, p827, p828, p829, p830, p831, p832, p833, p834, p835, p836, p837, p838, p839, p840, p841, p842, p843, p844, p845, p846, p847, p848, p849, p850, p851, p852, p853, p854, p855, p856, p857, p858, p859, p860, p861, p862, p863, p864, p865, p866, p867, p868, p869, p870, p871, p872, p873, p874, p875, p876, p877, p878, p879, p880, p881, p882, p883, p884, p885, p886, p887, p888, p889, p890, p891, p892, p893, p894, p895, p896, p897, p898, p899, p900, p901, p902, p903, p904, p905, p906, p907, p908, p909, p910, p911, p912, p913, p914, p915, p916, p917, p918, p919, p920, p921, p922, p923, p924, p925, p926, p927, p928, p929, p930, p931, p932, p933, p934, p935, p936, p937, p938, p939, p940, p941, p942, p943, p944, p945, p946, p947, p948, p949, p950, p951, p952, p953, p954, p955, p956, p957, p958, p959, p960, p961, p962, p963, p964, p965, p966, p967, p968, p969, p970, p971, p972, p973, p974, p975, p976, p977, p978, p979, p980, p981, p982, p983, p984, p985, p986, p987, p988, p989, p990, p991, p992, p993, p994, p995, p996, p997, p998, p999, p1000, p1001, p1002, p1003, p1004, p1005, p1006, p1007, p1008, p1009, p1010, p1011, p1012, p1013, p1014, p1015, p1016, p1017, p1018, p1019, p1020, p1021, p1022, p1023, p1024, p1025, p1026, p1027, p1028, p1029, p1030, p1031, p1032, p1033, p1034, p1035, p1036, p1037, p1038, p1039, p1040, p1041, p1042, p1043, p1044, p1045, p1046, p1047, p1048, p1049, p1050, p1051, p1052, p1053, p1054, p1055, p1056, p1057, p1058, p1059, p1060, p1061, p1062, p1063, p1064, p1065, p1066, p1067, p1068, p1069, p1070, p1071, p1072, p1073, p1074, p1075, p1076, p1077, p1078, p1079, p1080, p1081, p1082, p1083, p1084, p1085, p1086, p1087, p1088, p1089, p1090, p1091, p1092, p1093, p1094, p1095, p1096, p1097, p1098, p1099, p1100, p1101, p1102, p1103, p1104, p1105, p1106, p1107, p1108, p1109, p1110, p1111, p1112, p1113, p1114, p1115, p1116, p1117, p1118, p1119, p1120, p1121, p1122, p1123, p1124, p1125, p1126, p1127, p1128, p1129, p1130, p1131, p1132, p1133, p1134, p1135, p1136, p1137, p1138, p1139, p1140, p1141, p1142, p1143, p1144, p1145, p1146, p1147, 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p1863, p1864, p1865, p1866, p1867, p1868, p1869		

Affy Qualifier	Affy Name	accession	sum of Present Calls	4 of 6 present	Avg Freq RA	Std Dev RA	sum of 7 of 13 abs pres dec	Present in RA and Normal	Present in RA, Absent in Normal	Change in RA, Present in Normal	Name	Chromosome	Kinase or Phosphatase
38338_at	RRAS	AI201108	6	Pass	15.83	5.53	12	Pass	TRUE	FALSE	related RAS viral (r-ras) oncogene homolog; RRAS	19q13.3	
34892_at	TNFRSF10	AF016266	6	Pass	15.83	5.49	13	Pass	TRUE	FALSE	tumor necrosis factor receptor superfamily, member 10b; TNFRSF10B	8p22-p21	
38181_at	MMP11	X57766	6	Pass	11.33	4.41	11	Pass	TRUE	FALSE	matrix metalloproteinase 11 (stromelysin 3); KIAA0674	22q11.23	
31826_at	KIAA0674	AB014574	6	Pass	28.00	9.40	13	Pass	TRUE	FALSE	KIAA0674 protein, 9	9	
34347_at	DKFZP564	AL049955	6	Pass	22.67	5.24	13	Pass	TRUE	FALSE	DKFZP564J0123 protein, 3p21.2-24.2	3p21.2-24.2	
40076_at	TPD52L2	AF004430	6	Pass	22.67	11.27	13	Pass	TRUE	FALSE	tumor protein D52-like 2, TPD52L2	20q13.2-q13.3	
37967_at	D6S49E	AF000424	6	Pass	100.17	51.60	13	Pass	TRUE	FALSE	DNA segment on chromosome 6 (unique) 49 expressed sequence; D6S49E Homo sapiens LST1 mRNA	6p21.3	
37487_at	KIAA1093	AB029016	6	Pass	10.33	3.88	13	Pass	TRUE	FALSE	KIAA1093 protein, 22	22	
41522_at	MFNG	Z93096	6	Pass	10.33	3.72	13	Pass	TRUE	FALSE	maize fringe (Drosophila) homolog; MFNG	22q12	
36637_at	ANXA11	L19605	6	Pass	25.83	7.41	13	Pass	TRUE	FALSE	annexin A11, ANXA11	10q22-q23	
553_g_at	ARHGAP1	U02570	6	Pass	43.00	15.65	13	Pass	TRUE	FALSE	Rho GTPase activating protein 1; ARHGAP1		
32201_at	SSNA1	Z96932	4	Pass	19.50	7.19	8	Pass	TRUE	FALSE	Sjogren's syndrome nuclear autoantigen 1		
39180_at	FUS	S62140	6	Pass	47.83	13.29	13	Pass	TRUE	FALSE	fusion, derived from t(12;16) malignant liposarcoma; FUS	16p11.2	
1062_g_at	IL10RA	U00672	6	Pass	47.67	15.71	13	Pass	TRUE	FALSE	interleukin 10 receptor, alpha, IL10RA	11q23	
41375_at	UNK_AJ24	AJ245416	6	Pass	15.17	5.88	13	Pass	TRUE	FALSE	Homo sapiens LST1 mRNA		
36199_at	DAP	X76105	6	Pass	21.67	3.88	12	Pass	TRUE	FALSE	death-associated protein, DAP	5p15.2	
37345_at	CALU	AF013759	5	Pass	6.40	1.14	12	Pass	TRUE	FALSE	calumenin, CALU	7q32	
38657_s_at	CLTA	M20471	6	Pass	43.17	19.93	13	Pass	TRUE	FALSE	clathrin, light polypeptide (Lc3), CLTA	12q23-q24	
32490_at	CEACAM4	AC005955	5	Pass	9.00	2.92	7	Pass	TRUE	FALSE	carcinoembryonic antigen-related cell adhesion molecule 4, CEACAM4	19q13.2	
37739_at	SSRP1	M86737	6	Pass	16.50	4.55	13	Pass	TRUE	FALSE	structure specific recognition protein 1, SSRP1	11q12	
32806_at	BZRP	M36035	6	Pass	248.17	116.68	13	Pass	TRUE	FALSE	benzodiazepine receptor (peripheral), BZRP	22q13.31	
31891_at	CH13L2	U58515	6	Pass	6.33	1.51	9	Pass	TRUE	FALSE	chitinase 3-like 2, CH13L2	1p13.3	
31801_at	UNK_A180	AI08712	6	Pass	13.00	6.26	13	Pass	TRUE	FALSE	chitinase 3-like 2, CH13L2		
34787_at	NRD1	X93209	6	Pass	32.17	9.64	13	Pass	TRUE	FALSE	hardylin (N-arginine diester convertase), NRD1	1p32.2-p32.1	
36666_at	P4HB	M22806	6	Pass	77.17	21.94	13	Pass	TRUE	FALSE	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase, thymid homologue binding)	17q25	
39738_at	APOL	Z82215	6	Pass	152.17	26.57	13	Pass	TRUE	FALSE	small nuclear ribonucleoprotein polypeptide A, SNRPA		
40842_at	SNRPA	M60784	6	Pass	36.17	8.80	13	Pass	TRUE	FALSE	small nuclear ribonucleoprotein polypeptide A, SNRPA	19q13.1	

Affy Qualifier	Affy Name	accession	sum of Present Calls	4 of 6 present	Avg Freq RA	Std Dev RA	sum of 7 of 13 present	Present in RA and Normal	Present in RA, Absent in Normal	Avg Freq (Normal)	Fold Change RA / Normal	Name	Chromosome	Kinase or Phosphatase	
39551_at	UNK_N98	N98667	6	Pass	25.00	9.57	13	Pass	TRUE	FALSE	12.77	1.96	hypothetical protein; LOC51317		
35017_f_at	UNK_M80	M80469	6	Pass	129.67	39.72	13	Pass	TRUE	FALSE	66.23	1.96	Cluster Incl M80469 Human MHC class I HLA-J gene, exons 1-8 and complete cds		
894_g_at	E2-EPT	M91670	6	Pass	13.50	4.85	10	Pass	TRUE	FALSE	6.90	1.96	ubiquitin carrier protein, E2-EPT	17	
590_at	ICAM2	M32334	6	Pass	26.33	4.72	13	Pass	TRUE	FALSE	13.46	1.96	intercellular adhesion molecule 2, ICAM2	17q23-q25	
34346_at	PRKAG1	U42412	6	Pass	16.83	6.01	13	Pass	TRUE	FALSE	8.62	1.95	protein kinase, AMP-activated, gamma 1 non-catalytic subunit	12q12-q14	
39500_s_at	UNK_AL0	AL049299	5	Pass	8.40	2.70	10	Pass	TRUE	FALSE	4.30	1.95	NADH dehydrogenase (ubiquinone) Fe-S protein 6 (13kD) (NADH-coenzyme Q reductase)		
34865_at	NDUFS6	A1360249	5	Pass	9.60	4.34	12	Pass	TRUE	FALSE	4.92	1.95	major histocompatibility complex, class II, DM alpha, HLA-DMA		
37344_at	HLA-DMA	X62744	6	Pass	51.50	18.12	13	Pass	TRUE	FALSE	26.38	1.95	actin related protein 2/3 complex, subunit 4 (20 kD), ARPC4	6p21.3	
34692_r_at	ARPC4	AF006087	6	Pass	22.67	7.84	13	Pass	TRUE	FALSE	11.62	1.95	ATX1 (antioxidant protein 1, yeast) homolog 1, ATOX1	5q32	
41776_at	ATOX1	U70660	6	Pass	13.33	4.50	12	Pass	TRUE	FALSE	6.83	1.95	synaptotagmin 2, SYNGR2	17qter	
34885_at	SYNGR2	AJ002308	6	Pass	75.17	17.66	13	Pass	TRUE	FALSE	38.54	1.95	ubiquitin carrier protein, E2-EPT	17	
893_at	E2-EPT	M91670	5	Pass	7.80	1.79	9	Pass	TRUE	FALSE	4.00	1.95	MD-2 protein, MD-2	8	
33956_at	MD-2	AB018549	6	Pass	13.50	7.89	13	Pass	TRUE	FALSE	6.92	1.95	deletelyl-phosphate mannosyltransferase		
38725_s_at	DPM2	N36295	6	Pass	10.50	3.56	13	Pass	TRUE	FALSE	5.38	1.95	polypeptide 2, regulatory subunit, DPM2		
40928_at	DKFZP564	W26496	6	Pass	10.50	8.41	13	Pass	TRUE	FALSE	5.38	1.95	small inducible cytokine A3 (homologous to mouse q21)	17q11-q21	
39811_at	UNK_AA4	AA402538	6	Pass	26.83	8.45	13	Pass	TRUE	FALSE	13.77	1.95	Min-1a, SCYA3		
36103_at	SCYA3	D90144	6	Pass	6.33	2.80	12	Pass	TRUE	FALSE	3.25	1.95	polypyrimidine tract binding protein (heterogeneous nuclear ribonucleoprotein I), PTB	14q23-q24.1	
40593_at	PTB	X66975	6	Pass	64.00	23.03	13	Pass	TRUE	FALSE	32.85	1.95	Human BRCA2 region, mRNA sequence CC006		
1532_g_at	UNK_U50	U50535	6	Pass	16.33	3.44	13	Pass	TRUE	FALSE	8.38	1.95	granzyme M (lymphocyte cytotoxic granule protein 1), PTB	19p13.3	
32264_at	UNK_L23	L23134	5	Pass	29.60	14.67	10	Pass	TRUE	FALSE	15.20	1.95	chemokine (C-C motif) receptor 7, CCR7	17q12-q21.2	
1097_s_at	CCR7	L31584	6	Pass	44.33	27.45	13	Pass	TRUE	FALSE	22.77	1.95	U5 snRNP-specific protein (220 kD), ortholog of S cerevisiae Prp8p, PRP8	17p13.3	
35753_at	PRP8	AB007510	6	Pass	56.00	9.06	13	Pass	TRUE	FALSE	28.77	1.95	KIAA0397 gene product, KIAA0397		
36129_at	UNK_AB0	AB007857	6	Pass	25.00	4.69	13	Pass	TRUE	FALSE	12.85	1.95	anizyme inhibitor protease, seme, LOC51582, PRSS15		
33367_s_at	LOC51582	D88674	6	Pass	4.33	2.34	10	Pass	TRUE	FALSE	8.50	-1.96	#N/A	19p13.2,8	
AFFX-M2783(28SRNA5	M27830	M27830	6	Pass	9.17	6.01	13	Pass	TRUE	FALSE	18.46	-2.01	#N/A	#N/A	



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34642_at	YWHAZ	U28964	6	Pass	15.17	10.83	13	Pass	TRUE	FALSE	30.62	-2.02	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide, YWHAZ	2p25.2-p25.1	
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41659_at	SUP76H	U46691	4	Pass	4.50	2.38	2	Fail	FALSE	TRUE	1.50	suppressor of Ty (S.cerevisiae) 6 homolog, SUP76H	17q11.2	
36158_at	DCTN1	AF086947	5	Pass	7.80	1.92	5	Fail	FALSE	TRUE	2.60	dynein 1 (p150, Glued (Drosophila) homolog), DCTN1	2p13	
35936_g_at	CPT1B	Y08683	5	Pass	8.00	2.35	4	Fail	FALSE	TRUE	2.75	carnitine palmitoyltransferase I, muscle, CPT1B	22q13.33	
41458_at	KIAA0467	AB007936	4	Pass	14.50	5.20	1	Fail	FALSE	TRUE	5.00	KIAA0467 protein, muscle, CPT1B	1	
33719_at	UNK_AFO	AF010242	4	Pass	8.50	1.73	2	Fail	FALSE	TRUE	3.00	protease serine, 16 (thymus), PRSS16	6p21	
39306_at	PRSS16	AF052514	4	Pass	8.50	3.51	2	Fail	FALSE	TRUE	3.00	protease serine, 16 (thymus), PRSS16	6p21	
37365_at	HSJ1	X63368	4	Pass	7.75	2.22	4	Fail	FALSE	TRUE	2.75	heat shock protein, neuronal DNAI1-like 1, HSJ1	2q32-q34	
40951_at	UNK_ALO	AL049250	5	Pass	6.40	5.50	3	Fail	FALSE	TRUE	2.33			
41351_at	UNK_AAS	AA885106	4	Pass	26.25	7.85	6	Fail	FALSE	TRUE	9.83	carnitine palmitoyltransferase I, muscle, CPT1B	22q13.33	
35228_at	CPT1B	Y08682	5	Pass	9.60	2.88	5	Fail	FALSE	TRUE	3.60	carnitine palmitoyltransferase I, muscle, CPT1B	22q13.33	
40165_at	UNK_ABO	AB015345	6	Pass	5.33	1.63	5	Fail	FALSE	TRUE	2.00	neutrophil cytosolic factor 1 (47kD, chronic granulomatous disease, autosomal 1), NCF1	7q11.23	
40159_r_at	NCF1	M55067	6	Pass	70.83	52.24	5	Fail	FALSE	TRUE	26.80	neutrophil cytosolic factor 1 (47kD, chronic granulomatous disease, autosomal 1), NCF1	7q11.23	
39837_s_at	UNK_ACO	AC004877	4	Pass	14.50	8.74	4	Fail	FALSE	TRUE	5.50	complement component 2, C2	6p21.3	
33374_at	C2	L09708	4	Pass	5.25	0.96	1	Fail	FALSE	TRUE	2.00	complement component 2, C2	6p21.3	
2009_at	PTK2B	U33284	4	Pass	5.25	1.50	2	Fail	FALSE	TRUE	2.00	protein tyrosine kinase 2, beta, PTK2B	8p21.1	Kinase
41083_at	UNK_ACO	AC006276	4	Pass	5.25	1.71	3	Fail	FALSE	TRUE	2.00	SREBP CLEAVAGE-ACTIVATING PROTEIN, SCAP	3	
37656_at	SCAP	D83782	5	Pass	11.00	3.94	4	Fail	FALSE	TRUE	4.25	SREBP CLEAVAGE-ACTIVATING PROTEIN, SCAP	3	
100_g_at	RABGGT4	Y08200	5	Pass	9.40	4.16	3	Fail	FALSE	TRUE	3.67	Rab geranylgeranyltransferase, alpha subunit RABGGT4	14q11.2	
41648_at	CRAT	X78706	4	Pass	20.50	3.11	4	Fail	FALSE	TRUE	8.00	carnitine acetyltransferase, CRAT	9q34.1	
37977_at	PMS2L11	A1138834	4	Pass	7.25	3.30	6	Fail	FALSE	TRUE	2.83	posmitotic segregation increased 2-like 11, PMS2L11	7q	
37491_at	TAF2A	D90359	4	Pass	15.75	6.99	6	Fail	FALSE	TRUE	6.17	TATA box binding protein (TBP)-associated factor, RNA polymerase II, A, 250RD, TAF2A	Xq13.1	
31410_at	TAC1	AF023614	4	Pass	7.00	4.08	4	Fail	FALSE	TRUE	2.75	transmembrane activator and CAML interactor, TAC1		
37360_at	LY6E	U66711	5	Pass	50.80	41.61	2	Fail	FALSE	TRUE	20.00	lymphocyte antigen 6 complex, locus E, LY6E	8q24.3	
35434_at	MEF2D	L16794	6	Pass	6.33	1.75	6	Fail	FALSE	TRUE	2.50	MADS box transcription enhancer factor 2, polypeptide D (myocyte enhancer factor 2D), MEF2D	1q12-q23	
38971_r_at	NAF1	AJ011896	4	Pass	53.50	25.51	5	Fail	FALSE	TRUE	21.20	Nef-associated factor 1, NAF1	5q32-q33.1	
36958_at	ZYX	X95735	6	Pass	42.83	22.68	4	Fail	FALSE	TRUE	17.00	zyxin, ZYX	7q32	
34432_at	SH2D2A	AF051325	5	Pass	4.60	3.71	6	Fail	FALSE	TRUE	1.83	SH2 domain protein 2A, SH2D2A	1q21	

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35194_at	GPX2	X53463	4	Pass	5.00	1.63	1 Fail	FALSE	TRUE	2.00	2.50	glutathione peroxidase 2 (gastrointestinal); GPX2	14q24.1	
38276_at	NFKBIE	U91616	4	Pass	5.00	0.82	1 Fail	FALSE	TRUE	2.00	2.50	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon		
40191_s_at	UNK_A176	AI761647	5	Pass	5.00	2.00	1 Fail	FALSE	TRUE	2.00	2.50	KIAA0582 protein, 2	2	
35079_at	NB-3	AB003592	4	Pass	5.00	0.82	4 Fail	FALSE	TRUE	2.00	2.50	contactin 6, CNTN6	3p26-p25	
36598_s_at	INPPL1	L36818	6	Pass	9.17	4.07	6 Fail	FALSE	TRUE	3.67	2.50	inositol polyphosphate phosphatase-like 1, INPPL1	11q23	Phosphatase
35601_at	UNK_L006	L00022	6	Pass	16.83	9.47	6 Fail	FALSE	TRUE	6.83	2.46			
37719_at	MLF2	AF070539	4	Pass	11.00	3.56	2 Fail	FALSE	TRUE	4.50	2.44	myeloid leukemia factor 2, MLF2	12p13	
38464_at	GCSI	X87237	5	Pass	12.20	3.42	4 Fail	FALSE	TRUE	5.00	2.44	glucosidase 1, GCSI	2p13-p12	
40639_at	SCO2	AL021683	4	Pass	14.50	10.63	1 Fail	FALSE	TRUE	6.00	2.42	SCO (cytochrome oxidase deficient, yeast) homolog 2, SCO2	22q13.33	
41273_at	UNK_AL0	AL046940	4	Pass	6.25	0.50	5 Fail	FALSE	TRUE	2.60	2.40			
35961_at	UNK_AL0	AL049390	5	Pass	4.80	1.10	4 Fail	FALSE	TRUE	2.00	2.40			
38721_at	HBP1	W72733	6	Pass	8.50	1.22	5 Fail	FALSE	TRUE	3.60	2.36	ITMG-box containing protein 1, HBP1	7q31.1	
519_g_at	NR1H2	U07132	6	Pass	25.17	7.57	3 Fail	FALSE	TRUE	10.67	2.36	nuclear receptor subfamily 1, group H, member 2, NR1H2	19q13.3-19q13.3	
41127_at	SLC1A4	L14595	5	Pass	6.20	2.28	6 Fail	FALSE	TRUE	2.67	2.33	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4, SLC1A4	2p15-p13	
38340_at	KIAA0655	AB014555	4	Pass	12.75	3.20	6 Fail	FALSE	TRUE	5.50	2.32	huntingtin interacting protein-1-related, KIAA0655	12q24	
32177_s_at	GAPL	AC004084	4	Pass	9.25	2.22	2 Fail	FALSE	TRUE	4.00	2.31	GTPase activating protein-like, GAPL	7q22-q31.1	
736_t_at	POM121L	D87002	4	Pass	10.00	2.58	3 Fail	FALSE	TRUE	4.33	2.31			
1550_at	MAAT1	U19796	4	Pass	8.00	2.45	2 Fail	FALSE	TRUE	3.50	2.29	melanoma-associated antigen recognised by T lymphocytes, MAAT1		
37945_at	HBACH	U91316	4	Pass	6.25	1.71	4 Fail	FALSE	TRUE	2.75	2.27	cytosolic acyl coenzyme A thioester hydrolase, HBACH	1p36.31-p36.11	
31822_at	CUTL1	L12579	5	Pass	9.40	3.29	6 Fail	FALSE	TRUE	4.17	2.26	cut (Drosophila)-like 1 (CCAAAT displacement protein), CUTL1	7q22	
33105_at	UNK_W28	W28790	4	Pass	5.25	2.63	3 Fail	FALSE	TRUE	2.33	2.25			
35149_at	TNFRSF5	AI865431	4	Pass	6.75	3.59	6 Fail	FALSE	TRUE	3.00	2.25	tumor necrosis factor receptor superfamily, member 5, TNFRSF5	20q12-q13.2	
40619_at	E2-EPF	M91670	4	Pass	8.50	1.00	6 Fail	FALSE	TRUE	3.83	2.22	ubiquitin carrier protein, E2-EPF	17	
570_at	RELB	M83221	6	Pass	8.00	3.35	6 Fail	FALSE	TRUE	3.67	2.18	v-rel avian reticuloendotheliosis viral oncogene homolog B (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3), RELB		
1007_s_at	DDR1	U48705	4	Pass	6.00	3.37	4 Fail	FALSE	TRUE	2.75	2.18	discoidin domain receptor family, member 1, DDR1	6p21.3	Kinase
36856_at	UNK_W28	W28743	5	Pass	13.80	6.72	6 Fail	FALSE	TRUE	6.33	2.18			

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37754_at	LGALS3BP	L13210	4	Pass	3.25	1.50	4 Fail	FALSE	TRUE	1.50	2.17	lectin, galactoside-binding, soluble, 3 binding protein (galactin 6 binding protein), LGALS3BP	17q25	
33387_at	GAS7	AB007854	4	Pass	6.00	1.83	5 Fail	FALSE	TRUE	2.80	2.14	growth arrest-specific 7, GAS7	17p	
35960_at	IKBKB	AF031416	4	Pass	9.25	2.22	6 Fail	FALSE	TRUE	4.33	2.13	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta, IKBKB	8p11.2	Kinase
40359_at	C11ORF13	M91083	5	Pass	19.20	4.09	4 Fail	FALSE	TRUE	9.00	2.13	chromosome 11 open reading frame 13, C11ORF13	11p15.5	
1397_at	MAP3K11	L32976	4	Pass	4.25	1.50	3 Fail	FALSE	TRUE	2.00	2.13	mitogen-activated protein kinase kinase 11, MAP3K11	11q13.1-q13.3	Kinase
33528_at	KIAA0125	D50915	4	Pass	4.25	0.96	3 Fail	FALSE	TRUE	2.00	2.13	KIAA0125 gene product, KIAA0125		
38995_at	CLDN5	AF000959	4	Pass	14.00	3.74	5 Fail	FALSE	TRUE	6.60	2.12	claudin 5 (transmembrane protein deleted in velocardiofacial syndrome), CLDN5	22q11.21	
39891_at	UNK_A124	A1246730	4	Pass	12.00	3.56	6 Fail	FALSE	TRUE	5.67	2.12	transcription factor binding to IGJH enhancer	Xp11.22	Kinase
34669_at	TFE3	X96717	5	Pass	6.00	1.22	6 Fail	FALSE	TRUE	2.83	2.12	mitogen-activated protein kinase 3, MAPK3	16p11.2	Kinase
40925_at	UNK_AAS	AA554945	4	Pass	9.50	2.65	6 Fail	FALSE	TRUE	4.50	2.11	mitogen-activated protein kinase 3, MAPK3		
1000_at	MAPK3	X60188	6	Pass	7.33	3.08	6 Fail	FALSE	TRUE	3.50	2.10	KIAA0540 protein, KIAA0540	3p21.2-p21.1	
35763_at	UNK_AB0	AB011112	6	Pass	8.83	5.64	4 Fail	FALSE	TRUE	4.25	2.08	ammoniumhyaluronate (glycine cleavage system protein T), AMT		
41120_at	AMT	D14686	6	Pass	4.50	1.52	6 Fail	FALSE	TRUE	2.17	2.08	p450 (cytochrome) oxidoreductase, POR	7q11.2	
703_at	UNK_L235	L23566	4	Pass	14.50	9.98	3 Fail	FALSE	TRUE	7.00	2.07	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma, IKBKG	Xq28	
858_at	POR	S90469	4	Pass	7.75	3.30	4 Fail	FALSE	TRUE	3.75	2.07	KIAA1089 protein, KIAA1089	1	
1089.1_at	UNK_M64	M64936	4	Pass	2.75	1.50	3 Fail	FALSE	TRUE	1.33	2.06	procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VII)	1p36.3-p36.2	
36004_at	IKBKG	AF074382	4	Pass	15.75	3.86	3 Fail	FALSE	TRUE	7.67	2.05	integrin, alpha 5 (fibronectin receptor, alpha 5 polypeptide), ITGA5	12q11-q13	
34868_at	KIAA1089	AB029012	5	Pass	4.60	1.14	4 Fail	FALSE	TRUE	2.25	2.04	cystinosis, nephropathic, CTNS	17p13	
36184_at	PLOD	L06419	5	Pass	11.00	8.60	5 Fail	FALSE	TRUE	5.40	2.04	ondoglin (Osler-Rendu-Weber syndrome I), ENG	9q33-q34.1	
39753_at	ITGA5	X06256	4	Pass	9.50	4.65	3 Fail	FALSE	TRUE	4.67	2.04	interleukin 15 receptor, alpha, IL15RA	10p15-p14	
36566_at	CTNS	A1222967	4	Pass	4.00	1.41	1 Fail	FALSE	TRUE	2.00	2.00	KIAA0652 gene product, KIAA0652	11	
32562_at	ENG	X72012	4	Pass	8.00	2.71	3 Fail	FALSE	TRUE	4.00	2.00	carbonic anhydrase IV, CA4	17q23	
495_at	IL15RA	U31628	4	Pass	4.00	0.82	3 Fail	FALSE	TRUE	2.00	2.00	similar to S. cerevisiae SSM4; TEB4	5p15.2	
38020_at	KIAA0652	AB014552	5	Pass	4.80	2.39	5 Fail	FALSE	TRUE	2.40	2.00			
40739_at	CA4	M83670	5	Pass	6.00	1.87	6 Fail	FALSE	TRUE	3.00	2.00			
32802_at	TEB4	AB011169	6	Pass	8.67	4.50	6 Fail	FALSE	TRUE	4.33	2.00			

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36307_at	KIAA0278	D87468	5	Pass	12.80	4.55	4	Fail	FALSE	TRUE	6.50	1.97	activity-regulated cytoskeleton-associated protein, ARC	8q24.3	
35230_at	CL24751	AF070530	5	Pass	8.80	3.03	6	Fail	FALSE	TRUE	4.50	1.96	hypothetical protein, clone 24751, CL24751	19	
35411_at	ATP-BL	AB018551	6	Pass	12.50	4.68	5	Fail	FALSE	TRUE	6.40	1.95	ATP synthase, subunit b-like, A1P-BL	16q24	
37098_at	PPOX	D38537	5	Pass	7.80	2.05	5	Fail	FALSE	TRUE	4.00	1.95	protoporphyrinogen oxidase, PPOX	1q22	
37149_s_at	UNK_U95	U95G26	4	Pass	10.00	8.29	3	Fail	FALSE	TRUE	25.00	-2.50	lactoferrin, LTF	#N/A	

qualifier	name	Accession	sum of abs dec	4 of 6 present	Avg Freq	Std Dev	sum of 7 of 13 abs present	Present in RA and Normal	Present in RA, Absent in Normal	Avg Freq (Normal)	Fold Change RA/Normal	Name	Chromosome
1029_s_at	UNK_U07	U07794	0	Fail	#DIV/0!	#DIV/0!	7 Pass	FALSE	FALSE	2.43	#DIV/0!	TXK tyrosine kinase, TXK	4p12
31495_at	SCYC2	D63789	0	Fail	#DIV/0!	#DIV/0!	7 Pass	FALSE	TRUE	4.29	#DIV/0!	small inducible cytokine subfamily C, member 1 (lymphotactin), small inducible cytokine subfamily C, member 2; SCYC1 SCYC2	1q21-1q25, 1q23-q25
32319_at	TNFSF4	AL022310	0	Fail	#DIV/0!	#DIV/0!	7 Pass	FALSE	TRUE	10.00	#DIV/0!	tumor necrosis factor (ligand) superfamily, member 4 (tax- transcriptionally activated glycoprotein 1, 34kD), TNFSF4	1q25
32350_at	MALT1	AB026118	0	Fail	#DIV/0!	#DIV/0!	7 Pass	FALSE	TRUE	2.43	#DIV/0!	mucosa associated lymphoid tissue lymphoma translocation gene 1, MALT1	18q21
32539_at	COP9	U51205	0	Fail	#DIV/0!	#DIV/0!	7 Pass	FALSE	TRUE	5.29	#DIV/0!	COP9 homolog, COP9	
33410_at	ITGA6	S66213	0	Fail	#DIV/0!	#DIV/0!	7 Pass	FALSE	TRUE	2.29	#DIV/0!	integrin, alpha 6, ITGA6	2
34704_r_at	UNK_AA1	AA151971	0	Fail	#DIV/0!	#DIV/0!	7 Pass	FALSE	TRUE	3.57	#DIV/0!	HERV-H LTR-associating 1, HHLA1	8q24
34875_r_at	KIAA0203	D86958	0	Fail	#DIV/0!	#DIV/0!	7 Pass	FALSE	TRUE	2.57	#DIV/0!	KIAA0203 gene product, KIAA0203	8
36237_at	SLC22A6	AB009698	0	Fail	#DIV/0!	#DIV/0!	7 Pass	FALSE	TRUE	3.14	#DIV/0!	solute carrier family 22 (organic anion transporters), member 6, KYNLU	11q11
38492_at	KYNLU	D55639	0	Fail	#DIV/0!	#DIV/0!	7 Pass	FALSE	TRUE	3.14	#DIV/0!	kynureninase (L-kynurenine hydrolase); KYNLU	
38512_r_at	ELAVL3	D26158	0	Fail	#DIV/0!	#DIV/0!	7 Pass	FALSE	TRUE	22.71	#DIV/0!	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 3 (Hu antigen C), ELAVL3	19p13.2
40590_at	CDC27	AA166687	0	Fail	#DIV/0!	#DIV/0!	7 Pass	FALSE	TRUE	3.57	#DIV/0!	cell division cycle 27, CDC27	17q12-17q23.2
526_s_at	PMS2	U11696	0	Fail	#DIV/0!	#DIV/0!	7 Pass	FALSE	TRUE	2.71	#DIV/0!	postmeiotic segregation increased (S cerevisiae) 2, PMS2	7p22
AFEX-M2783/28SRNAM		M27830	0	Fail	#DIV/0!	#DIV/0!	7 Pass	FALSE	TRUE	39.14	#DIV/0!		
36411_s_at	ELAVL2	U29943	0	Fail	#DIV/0!	#DIV/0!	8 Pass	FALSE	TRUE	7.25	#DIV/0!	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2, ELAVL2	9p21

Ally Qualifier	Ally Name	accession	sum of Present Calls	4 of 6 present	Avg Freq RA	Std Dev RA	sum of 7 of 13 present abs dec	Present in RA and Normal	Present in RA, Absent in Normal	Absent in RA, Present in Normal	Avg Freq (Normal)	Fold Change RA / Normal	Name	Chromosome	Kinase or Phosphatase
38660_at	COX6A2	F27891	0	Fail	#DIV/0!	#DIV/0!	8 Pass	FALSE	FALSE	TRUE	2.63	#DIV/0!	cytochrome c oxidase subunit VIa polypeptide 2; COX6A2	16p	
32641_at	KIAA0979	AB023196	0	Fail	#DIV/0!	#DIV/0!	9 Pass	FALSE	FALSE	TRUE	2.56	#DIV/0!	protein, androgen-induced prostate proliferative shut-off associated protein, AS3 KIAA0979	13q12-13q13	
32941_at	ICSBP1	M91196	0	Fail	#DIV/0!	#DIV/0!	9 Pass	FALSE	FALSE	TRUE	8.22	#DIV/0!	interferon consensus sequence binding protein 1, ICSBP1		
148_at	ELL2	U88629	1	Fail	11.00	#DIV/0!	7 Pass	FALSE	FALSE	TRUE	3.71	2.96	ELL-RELATED RNA POLYMERASE II ELONGATION FACTOR, ELL2		
35590_s_at	GIPR	X81832	3	Fail	25.33	2.89	7 Pass	FALSE	FALSE	TRUE	9.43	2.69	gastric inhibitory polypeptide receptor, GIPR	19q13.3	
31559_at	SLC13A2	U26209	3	Fail	11.67	2.08	7 Pass	FALSE	FALSE	TRUE	4.43	2.63	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2, SLC13A2	17p11.1-q11.1	
34903_at	UNK_A101	A1017382	3	Fail	15.67	7.09	9 Pass	FALSE	FALSE	TRUE	6.22	2.52	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9 (39kD), NDUF9A		
36205_at	NDUF9A	L04490	1	Fail	11.00	#DIV/0!	7 Pass	FALSE	FALSE	TRUE	4.43	2.48	nucleolar cysteine-rich protein, HSA6591		
396_f_at	EPOR	X97671	2	Fail	29.50	0.71	9 Pass	FALSE	FALSE	TRUE	12.44	2.37	erythropoietin receptor, EPOR	19p13.3-p13.2	
34098_f_at	UNK_A173	A1799757	2	Fail	7.50	2.12	7 Pass	FALSE	FALSE	TRUE	3.29	2.28	keratin, hair, acidic, 3A, KRT14.3A	17q12-q21	
31594_at	KRTHA3A	Y16788	2	Fail	11.00	5.66	7 Pass	FALSE	FALSE	TRUE	4.86	2.26	corticotropin releasing hormone receptor 1, CRHR1	17q12-q22	
40651_s_at	CRHR1	AF039523	1	Fail	7.00	#DIV/0!	10 Pass	FALSE	FALSE	TRUE	3.10	2.26	G-protein coupled receptor, RE2		
40299_at	RE2	AF091890	2	Fail	35.50	13.44	8 Pass	FALSE	FALSE	TRUE	15.75	2.25	chondroitin 6-sulfotransferase-2, C6ST-2	Xp11	
33037_at	UNK_AL0	AL022165	1	Fail	7.00	#DIV/0!	8 Pass	FALSE	FALSE	TRUE	3.13	2.24	CLF-related factor, CRF	17q21	
39920_r_at	CRF	AF095154	3	Fail	93.33	14.05	10 Pass	FALSE	FALSE	TRUE	41.70	2.24	farnesyltransferase, CAA1	14q23-q24	
31586_f_at	UNK_X72	X72475	3	Fail	8.67	2.89	9 Pass	FALSE	FALSE	TRUE	3.89	2.23	growth differentiation factor 1, GDF1	17q21	
37488_at	FNTB	L00635	2	Fail	7.00	1.41	7 Pass	FALSE	FALSE	TRUE	3.14	2.23	forkhead box M1, FOXM1	12p13	
2047_s_at	JUP	M23410	3	Fail	17.33	9.29	8 Pass	FALSE	FALSE	TRUE	7.88	2.20	truncalcolide repeat containing 12, TNRC12	12qter	
888_s_at	GDF1	M62302	3	Fail	10.33	0.58	8 Pass	FALSE	FALSE	TRUE	4.75	2.18	erythroid differentiation and demyelination factor 1, HPL-EDDG1		
40622_r_at	UNK_AL0	AL096740	3	Fail	38.00	13.11	9 Pass	FALSE	FALSE	TRUE	17.56	2.16	topoisomerase (DNA) II beta (180kD), TOP2B	3p24	
41324_g_at	FOXM1	U90917	1	Fail	16.00	#DIV/0!	10 Pass	FALSE	FALSE	TRUE	7.50	2.13	putative receptor P2X, ligand-gated ion channel, P2RX7	12q24	
39844_at	UNK_A180	A1806379	2	Fail	8.00	2.83	12 Pass	FALSE	FALSE	TRUE	3.83	2.09			
34815_at	TNRC12	U80743	1	Fail	5.00	#DIV/0!	7 Pass	FALSE	FALSE	TRUE	2.43	2.06			
33493_at	HPL-EDDG1	AF048849	2	Fail	10.00	2.83	8 Pass	FALSE	FALSE	TRUE	4.88	2.05			
1581_s_at	UNK_M27	M27504	1	Fail	5.00	#DIV/0!	9 Pass	FALSE	FALSE	TRUE	2.44	2.05			
33697_at	P2RX7	Y12851	3	Fail	7.00	1.00	8 Pass	FALSE	FALSE	TRUE	3.50	2.00			
31503_at	UNK_W28	W28732	2	Fail	9.50	7.78	11 Pass	FALSE	FALSE	TRUE	4.82	1.97			

Affy Qualifier	Affy Name	accession	sum of Present Calls	4 of 6 present	Avg Freq RA	Std Dev RA	sum of abs dec	Present in RA and Normal	Present in RA, Absent in Normal	Absent in RA, Present in Normal	Avg Freq (Normal)	Fold Change RA / Normal	Name	Chromosome	Kinase or Phosphatase
718_at	PRSS11	D87258	2	Fail	4.50	0.71	7 Pass	FALSE	FALSE	TRUE	2.29	1.97	protease, serine, 11 (GF binding); PRSS11	10q25.3-q26.2	
38229_at	UNK_X90	X90579	3	Fail	92.33	20.98	7 Pass	FALSE	FALSE	TRUE	47.00	1.96			
393_s_at	RUNX1	X90976	2	Fail	5.00	0.00	11 Pass	FALSE	FALSE	TRUE	2.55	1.96	run-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene); RUNX1	21q22.3	
1170_at	CSF1	M37435	1	Fail	9.00	#DIV/0!	10 Pass	FALSE	FALSE	TRUE	4.60	1.96			
40490_at	DDX21	U41387	3	Fail	3.67	1.53	11 Pass	FALSE	FALSE	TRUE	7.82	-2.13	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 21; DDX21	#N/A	10

CIA PBMC data Fold changes are shown as normalized

TBS= total body score

TBS 0*	Control	Preat									Common	Genbank	EC	Description	Phenotype	Map	Keywords	Symbol
		TBS-1	TBS-2	TBS-3	TBS-4	TBS-5	TBS-6	TBS-7	TBS-8	TBS-9								
J03023	0	-1.62	1.08	-3.25	2.23	1.54	1.54	1.62			hemopoietic cell kinase; Hck	J03023	2.7.1.112	TYROSINE-KINASE HCK (EC 2.7.1.112) (P56-HCK AND P60-HCK) (HEMOPOIETIC CELL KINASE) (B-CELL/MYELOID KINASE)	EXPRESSED PREDOMINANTLY IN THE MYELOID AND B-LYMPHOID LINEAGES	2 86.0 cM	Hemostasis	Hck
AA028657	0	3.00	19.00	17.00	17.00	37.50	16.50	20.00			EST; Unknown	AA028657					EST; Unknown	Unknown
Msa.10146.0	0	1.80	12.40	13.80	13.60	19.60	15.20	19.20			vWF; human	AA168633					Hemostasis	
Msa.10146.0	0	1.80	12.40	13.80	13.60	19.60	15.20	19.20			vWF; human	AA168633					Hemostasis	
W62701	0	2.40	20.20	19.00	16.40	22.80	18.20	18.80				W62701						
W62701	0	2.40	20.20	19.00	16.40	22.80	18.20	18.80				W62701						
Msa.1497.0	0	1.50	7.00	5.50	6.00	11.00	6.50	15.50			calmodulin 3; Calm3	M19380	2.7.1.38			74.0 cM	Regulatory	Calm3
Msa.1497.0	0	1.50	7.00	5.50	6.00	11.00	6.50	15.50			calmodulin 3; Calm3	M19380	2.7.1.38			74.0 cM	Regulatory	Calm3
Msa.723.0	0	2.00	8.00	5.00	3.00	10.00	9.00	15.00			aquaporin 1; Aqp1	L02914		AQUAPORIN-CHIP (WATER CHANNEL PROTEIN FOR RED BLOOD CELLS AND KIDNEY PROXIMAL TUBULE) (AQUAPORIN 1) (EARLY RESPONSE	ERYTHROCYTES AND RENAL TUBULES.	6 27.0 cM	Cell Surface Protein	Aqp1
D16262	0	0.00	9.00	10.00	8.00	21.00	16.00	14.00			mesoderm specific transcript; Mest	D16262				6 7.5 cM	Cytokine	Mest



X15592	0	1.33	13.67	13.00	16.67	14.67	13.00	14.00	cytotoxic T lymphocyte-associated protein 2 beta; Cila2b	X15592		CILA-2-BETA PROTEIN PRECURSOR (FRAGMENT)	13 42.0 cM		Cila2b
Msa.3237.0	0	0.00	7.50	9.00	9.00	9.50	9.50	13.50	LIM domains I; Fhl1	W14830			X A6-A7.1	Regulatory	Fhl1
M87276	0	0.00	6.00	7.00	5.00	10.00	11.00	13.00	thrombospondin 1; Thbs1	M87276		THROMBOSPONDIN 1 PRECURSOR.	2 65.0 cM	Extracellular Protein	Thbs1
AA616664	0	0.00	10.75	11.00	10.00	16.75	12.00	11.25	von Willebrand Factor; vWF; homolog	AA616664				Hemostasis	vWF
W45778	0	1.27	8.47	9.40	9.00	9.53	8.00	9.27		W45778					
W64688	0	0.00	6.82	7.36	5.55	9.82	7.09	8.73		W64688				EST; Unknown	
ab000822	0	1.10	7.30	7.10	7.80	10.10	7.70	8.50	synaptosomal-associated protein, 23kD; Snap23	AB000822			2 61.8 cM		Snap23
M19380	0	0.00	4.67	4.00	5.33	9.00	6.67	8.33	calmodulin 3; Calm3	M19380	2.7.1.38		7 4.0 cM	Regulatory	Calm3
AA542220	0	-1.09	5.00	4.75	7.00	8.92	5.92	7.50	TBX1 protein; TBX1	AA542220		TBX1 PROTEIN (T-BOX PROTEIN 1) (TESTIS-SPECIFIC T-BOX		Intracellular Protein	TBX1
Msa 1160 0	0	0.00	7.67	2.00	7.67	2.00	5.33	5.67	serum amyloid A 3; Saa3	X03505		SERUM AMYLOID A-3 PROTEIN PRECURSOR.	7 23.5 cM	Extracellular Protein	Saa3
X03479	0	-1.20	6.17	1.50	5.17	1.67	3.50	5.17	serum amyloid A 3; Saa3	X03479		SERUM AMYLOID A-3 PROTEIN PRECURSOR.	7 23.5 cM	Extracellular Protein	Saa3
U92478	0	0.00	3.00	2.33	3.33	6.00	5.33	4.67	development and differentiation enhancing; Ddefl	U92478				Regulatory	Ddefl

Msa.3665.0	0	-1.12	3.33	4.00	3.67	5.44	4.67	4.67	DNA segment, Chr 2, Wayne State University 143, expressed; D2Wsu143e	AA116604				2 24.0 cM	Proteolytic	D2Wsu143e
D67016	0	-2.33	-1.75	-1.75	1.14	3.14	1.14	4.43	heat shock protein, 105 kDa; Hsp105	D67016			HEAT-SHOCK PROTEIN 105 MOST TISSUES. SHOCK-RELATED 100 EXPRESSED IN BRAIN.	5 88.0 cM		Hsp105
AA120653	0	-1.69	2.84	2.41	2.77	4.50	3.07	3.80	transgelin 2; Tagln2	AA120653				1 94.2 cM	Structural Protein	Tagln2
AA285502	0	-2.00	2.00	2.00	2.00	4.50	3.50	3.75	receptor (calcitonin) activity modifying protein 1; Ramp1	AA285502					Regulatory	Ramp1
U35124	0	-1.87	2.07	2.00	2.27	4.00	2.73	3.67	protein tyrosine phosphatase, non-receptor type 18; Ptpn18	U35124				1 17.3 cM	Regulatory	Ptpn18
U05837	0	-1.60	0.00	-1.14	1.75	2.25	2.00	3.50	hexosaminidase A; Hexa	U05837	3.2.1.52	BETA-HEXOSAMINIDASE ALPHA CHAIN PRECURSOR (EC 3.2.1.52) (N-ACETYL-BETA-GLUCOSAMINIDASE) (BETA-N-ACETYLHEXOSAMINIDASE)	9 29.0 cM	Proteolytic	Hexa	

U27830	0	-1.67	-2.50	-2.50	0.00	2.00	1.20	3.20	stress-induced phosphoprotein 1; Stip1	U27830							Stip1
Msa.4113.0	0	-1.50	1.44	1.22	2.78	1.33	2.44	3.11	glucocorticoid-induced leucine zipper; Gilz	AA050733						Signal Transduction	Gilz
C79010	0	-1.33	2.25	2.08	4.33	4.25	3.00	3.08	Src-associated adaptor protein; Saps	C79010						??	Saps
C79010	0	-1.33	2.25	2.08	4.33	4.25	3.00	3.08	Src-associated adaptor protein; Saps	C79010						??	Saps
Msa.16995.0	0	-1.27	2.79	2.64	5.29	3.07	2.57	3.04	arachidonate 5-lipoxygenase activating protein	W83564						Intracellular Protein	
M22479	0	-2.00	2.75	3.00	3.00	5.00	3.50	3.00	tropomyosin 2, beta; Tpm2	M22479						EST, Unknown	Tpm2
AA238483	0	-3.33	-2.00	-2.00	-1.25	-1.11	-1.11	2.90	CD8 antigen, beta chain; Cd8b	AA238483					6 30.5 cM		Cd8b
M27960	0	-2.00	1.17	-2.00	3.50	1.33	1.33	2.83	interleukin 4 receptor, alpha; Il4ra	M27960					7 62.0 cM	Receptor	Il4ra
AA033103	0	-1.33	1.75	1.50	2.75	3.25	1.50	2.75		AA033103							
AA261246	0	-1.47	2.71	2.61	4.14	4.57	2.89	2.71		AA261246							
AA104254	0	-6.00	-6.00	-6.00	-3.00	-6.00	-1.20	2.67	transcription factor 17; KID-1 (kinase induced by depolarization); rat	AA104254						Transcription Factor	KID-1

0	1.03	3.05	2.89	3.02	1.95	2.10	2.63	cytotoxic T lymphocyte-associated protein 2	alpha; Ctl2a	XI5591		CTLA-2-ALPHA PROTEIN PRECURSOR.		13 36.0 cM	Cell Surface Protein	Ctl2a
U88328	0	-1.33	1.88	1.50	4.88	2.38	2.63	inducible SH2-containing protein 3; Cish3	cytokine	U88328		CYTOKINE INDUCIBLE SH2-CONTAINING PROTEIN 3 (PROTEIN EF-10).			ECM (Matrix Prot)	Cish3
Msa.4067.0	0	-1.25	1.20	1.80	3.20	2.40	2.60	Sip1?		AA003876					Unknown	
AA289661	0	-1.75	1.90	2.05	3.86	3.76	2.57	EST; Unknown		AA289661					EST; Unknown	Unknown
AF003693	0	-1.39	2.56	2.00	3.36	3.64	2.56	syndecan binding protein; Sdcbp		AF003693						Sdcbp
AA184116	0	-2.00	2.50	3.00	4.30	3.80	2.50	homolog of Alpha-actinin (human)		AA184116					Structural Protein	
U71205	0	0.00	3.00	3.00	4.00	5.50	2.50	RAS-like protein expressed in many tissues; Rit		U71205					Transcription Factor	Rit
Msa.36175.0	0	-1.33	2.50	2.50	16.00	2.50	2.50			AA124453					EST; Unknown	
Msa.22134.0	0	0.00	1.50	0.00	7.50	1.50	2.50	Unknown		AA031158					EST; Unknown	
X56602	0	0.00	8.50	1.50	1.50	0.00	2.50	interferon-stimulated protein (15 kDa); Isg15		X56602					Cytokine	Isg15
UI9118	0	-2.00	-1.33	-4.00	-1.33	0.00	2.50	activating transcription factor 3; Atf3		UI9118						Atf3



D37837	0	-1.20	0.00	-1.29	3.39	1.28	1.39	2.06	plastin 2, L; Pis2	D37837		L-PLASTIN (LYMPHOCYTE CYTOSOLIC PROTEIN 1) (LCP-1) (65 KDA MACROPHAGE PROTEIN)				Pis2	Structural Protein
X81627	0	1.43	4.86	3.14	17.29	3.14	2.14	2.00	lipocalin 2; Len2	X81627		NEUTROPHIL GELATINASE-ASSOCIATED LIPOCALIN PRECURSOR (NGAL) (P25) (SV-40 INDUCED 24P3	2 27.0 cM			Len2	Extracellular Protein
Msa.2129.0	0	2.00	6.33	3.67	31.67	3.33	2.00	2.00	lipocalin 2; Len2	W13166		NEUTROPHIL GELATINASE-ASSOCIATED LIPOCALIN PRECURSOR (NGAL) (P25) (SV-40 INDUCED 24P3	2 27.0 cM			Len2	Extracellular Protein
U96687	0	0.00	1.47	-1.25	3.07	1.73	1.53	2.00	paired-Ig-like receptor A10; paired-Ig-like receptor A6; Pira10, Pira6	U96687				7		Pira10, Pira6	
U27838	0	-3.50	-1.40	-3.50	0.00	1.57	1.29	2.00	GPL-anchored membrane protein 1; Gpiap-pending	U27838						Gpiap-pending	
Msa 3234.0	0	-1.33	-2.00	-4.00	2.75	1.25	0.00	2.00	myosin If; Myo1f	X97650					17 17.5 cM	Myo1f	Structural Protein
AA032906	0	-9.00	-9.00	-9.00	-4.50	-1.50	-1.29	2.00	Homologous to GENESEQN:V 49566 (human)	AA032906							Patented; Novel
AA032906	0	-9.00	-9.00	-9.00	-4.50	-1.50	-1.29	2.00	Homologous to GENESEQN:V 49566 (human)	AA032906							Patented; Novel

AA271024	0	-4.00	-4.00	-6.00	-1.33	1.08	-1.09	1.92	small nuclear ribonucleoprotein D2 polypeptide (SNRPD2)	AA271024						Other	
Msa.31660.0	0	-1.58	1.37	1.07	3.07	1.20	1.53	1.87	CD53 antigen; Cd53	AA105582						Cell Surface Protein	Cd53
ET62056	0	-3.22	-1.76	-2.32	1.45	1.29	1.33	1.86	immunoglobulin rearranged kappa chain	ET62056						Extracellular Protein	
ab009287	0	-2.33	-3.50	-7.00	0.00	1.14	0.00	1.86	CD68 antigen; Cd68	AB009287						Cell Surface Protein	Cd68
AA241085	0	-4.00	1.17	1.08	1.42	2.08	1.67	1.83	GENESEQN/Z 34468 Mouse 15 kDa selenoprotein	AA241085							
AA020104	0	-3.25	-1.62	-1.30	1.23	1.62	1.23	1.77	glycosylation dependent cell adhesion molecule 1; Glycam1	AA020104							Glycam1
Msa.38664.0	0	-2.13	-1.06	-1.89	4.88	1.12	1.06	1.76		AA144469						EST; Unknown	

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X94353	0	-1.33	3.00	2.25	5.50	1.75	1.75	1.75	1.75	cathepin-like protein; Cnlp	X94353		CATHELIN-RELATED ANTIMICROBIAL PEPTIDE STOMACH, PRECURSOR (CRAMP) (CATHELIN-LIKE PROTEIN) (CLP).	EXPRESSED IN TESTIS, SPLEEN, STOMACH, AND INTESTINE. VERY LOW EXPRESSION FOUND IN HEART, LUNG AND SKELETAL MUSCLE. NO EXPRESSION IN BRAIN, KIDNEY OR LIVER.	9 61.0 cM	Metabolic	Cnlp
ET62844	0	-1.33	1.25	-1.33	3.13	1.75	1.38	1.75	1.75	paired-Ig-like receptor A10,paired-Ig-like receptor A6; PirA10,PirA6	ET62844					7 Receptor	PirA10,PirA6
U06119	0	-2.88	-1.64	-3.29	1.17	1.35	1.26	1.74	1.74	cathepsin H; CtsH	U06119	3.4.22.16	CATHEPSIN H PRECURSOR (EC 3.4.22.16) (CATHEPSIN B3) (CATHEPSIN BA).	WIDELY EXPRESSED WITH HIGHEST EXPRESSION FOUND IN NON-SKELETAL TISSUES. LOW LEVELS FOUND IN SKELETAL TISSUE.	9 50.0 cM	Proteolytic	CtsH
M35153	0	-1.75	1.29	1.29	3.71	1.71	2.00		1.71	lamin B1; Lmnb1	M35153		LAMIN B1.		18 29.0 cM	ECM (Matrix Prot)	Lmnb1
Msa.739.0	0	-1.04	2.08	1.17	5.63	1.79	1.33		1.71	haploglobin; Hp	M96827				8 55.0 cM	Extracellular Protein	Hp
AA445408	0	-5.00	-2.50	-10.00	-1.43	-1.43	1.20		1.70	H3 histone, family 3B; H3f3b	AA445408					Other	H3f3b



Msa.7498.0	0	-1.50	1.67	1.33	3.67	0.00	1.33	1.67	growth arrest and DNA-damage-inducible, gamma; Gadd45g	AA138777		GROWTH ARREST AND DNA-DAMAGE-INDUCIBLE PROTEIN GADD45 GAMMA (CYTOKINE RESPONSIVE			Regulatory	Gadd45g
Msa.1903.0	0	-3.63	-2.07	-4.83	1.03	-1.61	-1.38	1.66	histocompatibility 2, class II, locus Dma,histocompatibility 2, class II, locus Mb1,histocompatibility 2, class II, locus Mb2,proteosome (prosome, macropain) type 9 (large multifunctional protease 2); H2-DMa,H2-DMb1,H2-DMb2,Pmb9	U35323		CLASS II HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN PRECURSOR, CLASS II HISTOCOMPATIBILITY ANTIGEN, M BETA 1 CHAIN PRECURSOR (H2-M BETA 1 CHAIN),PROTEASOME CHAIN 7 PRECURSOR (EC 3.4.99.46) (MACROPAIN CHAIN 7) (MULTICATALYTIC ENDOPEPTIDASE	17 18.56 cM,17 18.57 cM,17 18.58 cM,17 18.59 cM	<input type="checkbox"/>	H2-DMa,H2-DMb1,H2-DMb2,Pmb9	
U96689	0	-1.06	1.59	1.29	3.18	1.94	1.65	1.65	paired-Ig-like receptor B; Pirb	U96689				7 1.0 cM	Receptor	Pirb
V01527	0	-3.55	-1.95	-4.33	0.00	-1.30	-1.11	1.62	histocompatibility 2, class II antigen A, beta 1; H2-Ab1	V01527		H-2 CLASS II HISTOCOMPATIBILITY ANTIGEN, A-D BETA CHAIN	17 18.64 cM	Cell Surface Protein	H2-Ab1	
AA285691	0	-3.29	-1.55	-2.32	1.37	1.37	1.01	1.61	cytohesin binding protein (Cbn)	AA285691					Cell Surface Protein	

X51829	0	-5.00	-2.50	-3.33	-1.25	-1.25	-1.11	1.60	myeloid differentiation primary response gene 116; Myd116	X51829		MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116.					Other	Myd116
AA185060	0	-3.50	-2.33	-2.33	0.00	1.29	0.00	1.57	GENESEQN:Z52941 Human prostate tumor cDNA library derived EST fragment #84	AA185060							Unknown	
U59488	0	-1.75	-2.33	-3.50	1.43	-1.17	0.00	1.57	neutrophil cytosolic factor 4, Ncf4	U59488		NEUTROPHIL CYTOSOL FACTOR 4 (NCF-4) (NEUTROPHIL NADPH OXIDASE FACTOR 4) (P40-PHOX) (P40PHOX).		15 47.2 cM		Intracellular Protein	Ncf4	
L37297	0	-2.00	3.00	2.00	20.75	2.50	2.00	1.50	neutrophilic granule protein; Ngp	L37297						Intracellular Protein	Ngp	
L37297	0	-2.00	3.00	2.00	20.75	2.50	2.00	1.50	neutrophilic granule protein; Ngp	L37297						Intracellular Protein	Ngp	
D73368	0	-4.00	-3.00	-6.00	-1.20	1.08	0.00	1.50	enhancer of rudimentary homolog (Drosophila); Erh	D73368		DEAD-BOX PROTEIN 3 (DEAD-BOX RNA HELICASE DEAD3) (MDEAD3) (EMBRYONIC RNA HELICASE) (DIPASI) RELATED.	DEVELOPMENTALLY REGULATED.			Other	Erh	
K01923	0	-3.75	-1.54	-2.92	-1.14	1.04	1.03	1.50	histocompatibility 2, class II antigen A, alpha; H2-Aa	K01923		H-2 CLASS II HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN		17 18.65 cM		Cell Surface Protein	H2-Aa	

Msa.1700.0	0	-1.37	1.36	-1.29	3.14	1.32	1.09	1.45	phospholipase A2 group VII (platelet-activating factor acetylhydrolase, plasma); Pla2g7	U34277	3.1.1.47	PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (EC 3.1.1.47) (PAF ACETYLHYDROLASE) (PAF 2- ACYLHYDROLASE) (LDL- ASSOCIATED PHOSPHOLIPASE A2) (LDL- PLA(2)) (2- ACETYL-1- ALKYLGLYCEROPHOSPHOCHOLINE ESTERASE) (1-ALKYL-2- ACETYLGLYCEROPHOSPHOCHOLINE	PLASMA.	Cytokine	Pla2g7
C76739	0	-1.29	1.33	1.33	3.44	2.11	1.78	1.44	macrophage C-type lectin; Mpc1	C76739				Cell Surface Protein	Mpc1
U29947	0	-2.29	-1.78	-4.00	1.44	1.19	1.13	1.44	mannosidase 2, alpha B1; Man2b1	U29947		LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (EC 3.2.1.24) (MANNOSIDASE, ALPHA B) (LYSOSOMAL L ACID		Regulatory	Man2b1

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AA008321	0	-1.75	-1.75	-3.50	1.43	1.86	0.00	1.43	1.43	1.43	1.43	proteasome (prosome, macropain) subunit, alpha type 4; Psm4	AA008321	3.4.99.46	PROTEASOM E COMPONENT C9 (EC 3.4.99.46) (MACROPAIN SUBUNIT C9) (MULTICATALYTIC ENDOPEPTIDASE)			Proteolytic	Psm4
T25659	0	-3.50	-1.40	-2.33	1.14	1.14	0.00	1.43	1.43	1.43	1.43	heterogeneous nuclear ribonucleoprotein A2/B1; Hnpa2b1	T25659		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS A2/B1 (HNRNP A2)			EST; Unknown	Hnpa2b1
AA638408	0	-3.40	-2.83	-4.25	-1.42	-1.31	-1.13	1.41	1.41	1.41	1.41	arginine N-methyltransferase 1; Mmt1	AA638408					Signal Transduction	Mmt1
AA408475	0	-3.33	-2.50	-2.50	-1.11	1.50	1.30	1.40	1.40	1.40	1.40	ribosomal protein L13a; Rpl13a	AA408475		60S RIBOSOMAL PROTEIN L13A (TRANSPANTATION ANTIGEN P198) (TUM-P198)		7 25.0 cM	Intracellular Protein	Rpl13a
M59378	0	-3.25	-1.86	-3.25	-1.18	1.08	-1.30	1.38	1.38	1.38	1.38	tumor necrosis factor receptor superfamily, member 1b; Tnfrsf1b	M59378		TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TNF-R2) (P75)		4 75.5 cM	Receptor	Tnfrsf1b
AA189914	0	-1.26	2.08	2.83	2.79	3.92	2.38	1.38	1.38	1.38	1.38	cytidine monophosphate-N-acetylneuraminic acid synthetase; Cmas	AA189914				6 74.0 cM		Cmas
AA261402	0	-2.78	-1.92	-3.57	1.04	1.24	-1.14	1.36	1.36	1.36	1.36	EST; Unknown	AA261402					EST; Unknown	Unknown

\*



AA174982	0	-2.37	-1.76	-3.10	1.17	1.11	-1.17	1.36	coronin, actin binding protein 1A; Corola	AA174982		CORONIN-LIKE PROTEIN P57 (CORONIN 1A)	7 62.5 cM	Intracellular Protein	Corola
AA182228	0	-2.56	-3.29	-7.67	-1.15	-1.21	-1.28	1.35	EST; Unknown	AA182228				EST; Unknown	Unknown
AF032466	0	-1.50	2.33	1.67	6.00	2.33	1.33	1.33	arginase type II; Arg2	AF032466	3.5.3.1	ARGINASE II PRECURSOR (EC 3.5.3.1) (NON-HEPATIC ARGINASE) (KIDNEY-TYPE)			Arg2
AA152590	0	-3.00	-2.25	-4.50	-1.29	1.44	1.11	1.33	eukaryotic translation initiation factor 4A1; Eif4a1	AA152590			11 39.0 cM	Translation Factor	Eif4a1
AA273932	0	-3.57	-2.08	-2.78	-1.19	1.08	-1.09	1.32	aldo-keto reductase; LOC56043	AA273932				Other	LOC56043
AA189758	0	-3.25	-1.86	-3.25	-1.18	1.08	1.15	1.31	Wbscr5 gene product; Wbscr5	AA189758				Regulatory	Wbscr5
Msa.4530.0	0	-2.88	-1.92	-3.83	0.00	-1.15	-1.15	1.30	EST; region of homology to GENESEQN:Z 77537 Human ovarian tumor cDNA library derived EST fragment 88	AA106931				EST; Unknown	
K01925	0	-3.84	-1.66	-3.31	-1.16	-1.10	-1.10	1.30	histocompatibility 2, class II antigen A, alpha; H2-Aa	K01925		H-2 CLASS II HISTOCOMPATIBILITY ANTIGEN, A-K ALPHA CHAIN	17 18.65 cM	Hemostasis	H2-Aa

DI0911	0	-1.27	1.93	1.57	4.50	2.00	1.64	1.29	a disintegrin and metalloprotease domain (ADAM) 8; Adam8	DI0911	3.4.24.-	ADAM 8 PRECURSOR (EC 3.4.24.-) (A DISINTEGRIN AND METALLOPROTEINASE DOMAIN 8) (CELL SURFACE ANTIGEN MS2) (MACROPHAGE CYSTEINE-RICH	MACROPHAGE F3-F5 ES.	Proteolytic	Adam8
M59821	#####	-3.15	-5.13	-5.86	-1.58	-1.78	-1.58	1.27	immediate early response 2; Ier2	M59821		T-LYMPHOCYTE ACTIVATED PROTEIN (CYCLOHEXIMIDE-INDUCED) (CHX1) (IMMEDIATE EARLY		Intracellular Protein	Ier2
AA575696	0	-3.00	-3.00	-4.00	1.33	1.17	1.08	1.25	sorting nexin 1; Snx1	AA575696				Regulatory	Snx1
AA575696	0	-3.00	-3.00	-4.00	1.33	1.17	1.08	1.25	sorting nexin 1; Snx1	AA575696				Regulatory	Snx1
AA172851	0	-1.26	2.24	1.66	5.66	2.17	1.41	1.21	EST; Unknown	AA172851				EST; Unknown	Unknown
AA285635	0	-3.00	-2.40	-6.00	-1.33	1.17	-1.71	1.17	ectoplacental cone, invasive trophoblast giant cells, extraembryonic ectoderm and chorion sequence 21; Epcs21-pending	AA285635				EST; Unknown	Epcs21-pending
AA254740	0	-3.75	-1.67	-2.50	-1.15	1.13	0.00	1.13	Nop10p (human)	AA254740				Other	



AA407584	0	-4.00	-2.00	-3.00	-2.00	-1.09	-1.33	-1.20	DNA segment, Chr 7, Wayne State University 30, expressed,nucl eosome assembly protein 1-like 4; D7Wsu30e,Na p114	AA407584					7 69.0 cM,7 69.55 cM		D7Wsu30e	
AA529094	0	-3.33	-2.50	-3.33	-1.43	-1.25	-1.11	-1.25	extracellular proteinase inhibitor; Expi	AA529094								Expi
X93037	0	-1.50	-1.50	-1.50	3.33	0.00	-1.50	-1.50	early growth response 1; Egr1	X93037	WDNM1 PROTEIN PRECURSOR.							
M22326-2	0	-6.00	-4.40	-11.00	-6.00	-2.64	-3.88	-1.69		M22326	EARLY GROWTH RESPONSE PROTEIN 1 (EGR-1) (KROX-24 PROTEIN)				18 16.0 cM	Intracellular Protein	Egr1	



## CIA-001,011,012pawsU-FC

Raw data from GEDS Fold Change, Genes were originally filtered for Present/Absent using frequency data

Note here

Note here Note here Score (*) Systematic	control		prearth		Score 1		Score 2		Score 3		Score 4		Common	Genbank	description	function	Map	Keywords	Kinase or Phosphatase	
	C	Raw	P	Raw	StdErr	Raw	StdErr	Raw	StdErr	Raw	StdErr	Raw								StdErr
D37801	1.00	-1.13	-2.72	0.68	-1.99	0.15	-2.79	0.82	-2.51	0.14	protein tyrosine phosphatase, non-receptor type 21; Ptpn21	D37801	protein tyrosine phosphatase, non-receptor type 21 (ec 3.1.3.48) (protein-tyrosine phosphatase ptp-rl10)	may be involved in the regulation of growth and differentiation of liver cells.				Phosphatase		
AA204199	1.00	2.86	-3.91	2.24	-0.03	1.37	-2.26	0.12	-2.68	0.30	protein tyrosine phosphatase-493; Ptp493	AA204199		northern blot analysis revealed that prl-2 is preferentially expressed in skeletal muscle, while prl-3 is preferentially expressed in both skeletal muscle and heart, although both prl-2 and prl-3 are expressed at lower levels in other tissues		Signal Transduction	Phosphatase			
U28244	1.00	-1.70	-1.41	1.43	-0.79	1.88	-6.34	2.53	-6.56	1.87	phospholipase A2, group IIA (platelets, synovial fluid); Pla2g2a	U28244	phospholipase a2, membrane associated precursor (ec 3.1.1.4) (phosphatidylcholine 2-acylhydrolase) (group ii phospholipase a2) (enhancing factor) (af)	pa2 catalyzes the calcium-dependent hydrolysis of the 2-acyl groups in 3-sn-phosphoglycerides.	4 68.0 cM		Phosphatase			
Msa.30443.0	1.00	1.21	2.19	0.78	2.28	0.60	9.18	1.92	11.29	3.33	RAS-related C3 botulinum substrate 2; Rac2	AA097231	ras-related c3 botulinum toxin substrate 2 (p21-rac2) (en-7 protein).	function: seems to be involved in the regulation of the nadph oxidase. subcellular location: cytoplasmic; membrane-associated when activated. tissue specificity: hematopoietic specific. similarity: belongs to the small	Intracellular Protein	Kinase				

J03023	hemopoietic cell kinase; Hck	J03023	tyrosine-protein kinase hck (ec 2.7.1.112) (p56-hck and p60-hck) (hemopoietic cell kinase) (bcr-kinase) (myeloid kinase) (bcrk).	may serve as part of a signaling pathway coupling the fε receptor to the activation of the respiratory burst. may also contribute to neutrophil migration and may regulate the degranulation process of neutrophils.	286.0 cM	Hemostasis	Kinase	*
X06368	colony stimulating factor 1 receptor; Csf1r	X06368	macrophage colony stimulating factor 1 receptor precursor (csf-1-r) (ec 2.7.1.112) (fms proto-oncogene) (c-fms).	this protein is the receptor for csf-1, it is a protein tyrosine-kinase transmembrane receptor.	1830.0 cM	Cytokine	Kinase	*
Msa.1709.0	elastin; Eln	U08210	elastin precursor (tropoelastin).	major structural protein of tissues such as aorta and nuchal ligament, which must expand rapidly and recover completely.	575.0 cM		Kinase	*
Msa.6386.0	mitogen activated protein kinase 13; Mapk13	W13523			17A3-B		Kinase	*
Msa.1160.0	serum amyloid A 3; Saa3	X03505	serum amyloid a-3 protein precursor.	member of "a" family of apolipoproteins that are differentially expressed. some represent acute phase proteins in the response to inflammatory stimuli. one acts as a precursor of the amyloid a protein, a major constituent of amyloid fibrils.	723.5 cM	Extracellular Protein		*

X03479	1.00	-1.29	13.98	9.47	18.92	17.89	104.27	16.64	92.13	20.20	serum amyloid A 3; Saa3	X03479	serum amyloid a-3 protein precursor.	serum amyloid a proteins (saa) constitute a family of apolipoproteins that are differentially expressed. some family members represent acute phase proteins in the response to inflammatory stimuli. one of these acts as a	7 23.5 cM	Extracellular Protein	
U73004	1.00	4.48	15.01	7.85	9.35	4.84	56.63	17.17	86.24	20.61	secretory leukocyte protease inhibitor; Slpi	U73004	antileukoprotease 1 precursor (alp) (secretory leukocyte protease inhibitor).	acid-stable proteinase inhibitor with strong affinities for trypsin, chymotrypsin, elastase, and cathepsin g. may prevent elastase-mediated damage to oral and possibly other mucosal tissues. associated with wound healing due to its inhibition of		Proteolytic	
M83219	1.00	8.84	25.35	7.26	17.08	10.37	45.22	2.88	62.94	10.24	S100 calcium-binding protein A9 (calgranulin B); S100a9	M83219	calgranulin b (migration inhibitory factor-related protein 14) (mrp-14) (p14) (leukocyte 11 complex heavy chain)	expressed by macrophages in acutely inflamed tissues and in chronic inflammations. seems to be an inhibitor of protein kinases. also expressed in epithelial cells constitutively or induced during dermatoses. may interact with	3 43.6 cM	Cytokine	
U27267	1.00	1.00	9.77	7.32	6.29	5.29	46.55	3.12	52.23	16.41	small inducible cytokine B subfamily, member 5; Scyb5	U27267	small inducible cytokine b5 precursor (cytokine lix).	may participate in the recruitment of inflammatory cells by injured or infected tissue. involved in neutrophil activation	5 53.0 cM	Cytokine	

Msa.2129,0	1.00	2.49	9.94	3.74	4.24	3.09	49.39	3.66	45.88	11.97	lipocalin 2; Lcn2	W13166	neutrophil gelatinase-associated lipocalin precursor (ngal) (p25) (sv-40 induced 24p3 protein).	acute phase forms a covalently linked, disulfide-bridged heterodimer with the 92 kd type v collagenase (mmp-9). neutrophil gelatinase-associated lipocalin 2,25kda, found at moderate levels, only in breast and lung. component of human tear (lipophilic ligand carrier protein suprefamily, lipocalin family, kernal group), modulator of inflammation, involved in the	2 27.0 cM	Extracellular Protein	
J04596	1.00	1.16	6.78	5.34	3.06	1.86	25.23	2.49	37.61	11.33	GRO1 oncogene; Gro1	J04596	growth regulated protein precursor (platelet-derived growth factor-inducible protein kc) (secretory protein n51).	has chemotactic activity for neutrophils. contributes to neutrophil activation during inflammation (for similarity)	5 51.0 cM	Extracellular Protein	
Z27231	1.00	2.87	3.52	2.37	10.54	8.59	22.63	6.04	32.08	4.73	matrix metalloproteinase 9; Mmp9	Z27231	92 kda type iv collagenase precursor (ec 3.4.24.35) (92 kda gelatinase) (matrix metalloproteinase-9) (mmp-9) (gelatinase b) (gelb).	regulator in matrix remodeling, expressed in alveolar macrophages and granulocytes, key regulator of growth plate angiogenesis and apoptosis of hypertrophic chondrocytes in mice, and involved in the	2 96.0 cM	Metabolic	
M15131	1.00	1.55	5.35	3.53	5.53	4.53	28.75	3.16	31.62	8.61	interleukin 1 beta; Il1b	M15131	interleukin-1 beta precursor (il-1 beta).	produced by macrophages and monocytes, it is required for the interaction between antigen-presenting cells and lymphocytes initiating an immune response. it can also be produced from a number of other cells and is involved in a	2 73.0 cM	Cytokine	

X66402	1.00	-1.04	3.76	3.44	6.56	7.79	26.89	1.34	30.00	4.34	matrix metalloproteinase 3; Mmp3	X66402	stromelysin-1 precursor (ec 3.4.24.17) (matrix metalloproteinase-3) (mmp-3) (transin-1) (sl-1).	the stromelysins are metalloproteinase enzymes (ec 3.4.24.17) involved in the metabolism of the components of the extracellular matrix.	9 1.0 cM	Proteolytic	
AA638539	1.00	1.84	7.52	3.14	1.82	0.25	14.69	4.30	26.78	8.36	DNA segment, Chr 5, Wayne State University 111, expressed; D5Wsu111e	AA638539	insulin-like growth factor binding protein 4 precursor (igfbp-4) (ibp-4) (igf binding protein 4).	igf-binding proteins prolong the half-life of the igfs and have been shown to either inhibit or stimulate the growth promoting effects of the igfs on cell culture. they alter the interaction of igfs with their cell surface receptor.	5 54.0 cM	EST; Unknown	
Msa.27241.0	1.00	1.00	3.58	2.53	4.68	0.44	14.73	7.02	23.04	4.95	insulin-like growth factor binding protein 4; Igfbp4	AA066368	granulocyte colony stimulating factor (granulocyte); Csf3r	receptor for granulocyte colony-stimulating factor (g-csf). in addition it may function in some adhesion or recognition events at the cell surface.	4 57.5 cM	Receptor	
M58288	1.00	1.00	4.46	2.99	2.92	1.92	23.86	0.91	21.79	6.27	colony stimulating factor 3 receptor (granulocyte); Csf3r	M58288	tartrate-resistant acid phosphatase type 5 precursor (ec 3.1.3.2) (tr- ap) (tartrate-resistant acid atpase) (tramase)	aka trap (in mouse, not human) -- a lysosomal enzyme and marker of osteoclasts.	9 6.0 cM	Intracellular Protein	
M99054	1.00	1.38	2.39	1.33	14.56	12.33	20.35	11.20	21.54	4.48	acid phosphatase 5; tartrate resistant (TRAP); Acp5	M99054	calgranulin a (migration inhibitory factor-related protein 8) (mrp-8) (p8) (leukocyte 11 complex light chain) (chemotactic cytokine cp-10) (pro-inflammatory s100 cytokine).	expressed by macrophages in chronic inflammations. also expressed in epithelial cells constitutively or induced during dermatoses. may interact with components of the intermediate filaments	3 43.6 cM	Cytokine	
M83218	1.00	9.16	8.77	1.81	9.30	6.50	15.39	2.10	20.18	0.81	S100 calcium binding protein A8 (calgranulin A); S100a8	M83218					



X94353	1.00	4.36	6.28	1.96	3.34	0.80	3.60	1.19	14.16	0.37	cathelein-like protein; Cnlp	X94353	cathelein-related antimicrobial peptide precursor (cramp) (cathelein-like protein) (cln).	acts as a potent antimicrobial peptide.	9 61.0 cM	Metabolic	
Msa.38664.0	1.00	1.00	3.40	0.91	2.76	1.76	5.71	1.59	13.90	3.18		AA144469				EST; Unknown	
W49204	1.00	1.24	7.53	2.19	6.24	4.95	7.85	4.84	13.67	4.24	glypican 1; Gpc1	W49204	collagenase 3 precursor (ec 3.4.24.1) (matrix metalloproteinase-13) (mmp-13).	degrades collagen type I. does not act on gelatin or casein. could have a role in tumoral process. regulator of matrix remodeling component of the mmp cluster. expressed in the synovial membrane and synovial	9	Proteolytic	
X66473	1.00	1.79	0.70	1.41	2.92	4.00	10.73	1.24	13.46	1.70	matrix metalloproteinase 13; Mmp13	X66473					
L37297	1.00	2.53	6.23	1.63	2.38	0.66	3.08	1.11	12.74	1.56	neutrophilic granule protein; Ngp	L37297		a novel myeloid-specific granule protein related to porcine cathelin, but showing important structural differences. this may represent the first isolated member of a new cystatin family. more importantly, the small size of the protein binds to P- and L-selectins, the calcium-dependent high affinity interaction with p-selectin mediates the tethering and rolling of neutrophils and leukocytes on endothelial cells.		Intracellular Protein	
X91144	1.00	2.10	3.53	1.24	4.04	2.92	10.33	0.54	12.68	2.95	selectin, platelet (p-selectin) ligand; Selp1	X91144	p-selectin glycoprotein ligand 1 precursor (psgl-1) (selectin p ligand).	binds to P- and L-selectins, the calcium-dependent high affinity interaction with p-selectin mediates the tethering and rolling of neutrophils and leukocytes on endothelial cells.	5 64.0 cM	Extracellular Protein	
X54542	1.00	1.37	2.99	1.71	1.36	0.24	8.15	2.35	12.39	3.14	interleukin 6; Il6	X54542	interleukin-6 precursor (il-6) (interleukin hp-1) (cell hybridoma growth factor).	il6 may be the most extremely pleiotropic of cytokines, with a broad range of activities on different cell types.	5 17.0 cM	Cytokine	

X81627	lipocalin 2; Lcn2	2.91	11.79	0.13	12.19	0.96	2.57	1.14	3.27	1.92	1.00		neutrophil gelatinase-associated lipocalin precursor (ngal) (p25) (sv-40 induced 24h)	capable of carrying small lipophilic molecules like retinol, steroids, and odorants.	2 27.0 cM	Extracellular Protein		*
ET62052	immunoglobulin heavy chain 4 (serum IgG1); IgH-4	0.43	11.69	1.29	3.52	0.87	3.73	2.14	5.14	1.06	1.00				12 58.0 cM			
W44075	myeloperoxidase; Mpo	2.21	11.54	1.14	3.35	1.18	3.25	2.30	5.43	1.61	1.00		myeloperoxidase precursor (ec 1.11.1.7) (mmpo).	this enzyme is present in primary granules of neutrophils and plays a major role in the oxygen- dependent microbicidal system of granulocytes	11 49.0 cM	Intracellular Protein		*
Msa.6242.0	cathepsin K; Ctsk	1.01	10.59	2.31	8.04	3.18	4.33	2.37	-1.10	-1.69	1.00		cathepsin k precursor (ec 3.4.22.38).	closely involved in osteoclastic bone resorption and may participate partially in the disorder of bone remodeling. displays potent endoprotease activity against fibrinogen at acid ph. may play an important role in extracellular matrix degradation	3 47.9 cM	Proteolytic		*
U59488	neutrophil cytosolic factor 4; Ncf4	2.50	9.98	1.48	12.29	0.01	2.49	0.99	2.63	1.09	1.00		neutrophil cytosol factor 4 (ncf-4) (neutrophil nadph oxidase factor 4) (p40-phox) (p40phox).	nadph oxidase consists of proteins p47-phox, p67-phox, p4-phox, and a small regulatory g protein. p4-phox is not required for oxidase activity and has been proposed to have a regulatory function	15 47.2 cM	Intracellular Protein		*
Z12297	small inducible cytokine A7; Scya7	1.82	9.42	0.57	14.05	4.30	2.47	1.52	2.36	-1.13	1.00		small inducible cytokine a7 precursor (monocyte chemoattractant protein 3) (mcp-3) (monocyte chemoattractant protein 3) (interferine/chemokine precursor) (fcr)	chemotactic factor that attracts monocytes and eosinophils, but not neutrophils. augments monocyte anti-tumor activity (by similarity). also induces release of gelatinase b. binds to ccr1, ccr2, ccr3.	11 46.5 cM	Cytokine		*



C76739	1.00	1.00	1.85	1.03	2.46	3.48	12.67	2.14	9.30	2.34	macrophage C-type lectin; Mpc1	C76739		a type ii transmembrane protein with a single extracellular c-type lectin domain. expressed in cell lines and normal mouse tissues in a macrophage-restricted manner	656.5 cM	Cell Surface Protein	
U60438	1.00	1.09	2.36	0.99	2.45	1.31	17.95	6.58	8.54	2.10	serum amyloid A 2; Saa2	U60438	serum amyloid a-2 protein precursor [contains: amyloid protein a (amyloid fibril protein aa)].	saal, saa2, and saa3 encode acute phase response proteins in response to inflammatory stimuli. acts as a precursor of the amyloid a protein that is a major constituent of amyloid fibrils formed in secondary amyloidosis.	723.5 cM	Other	
X94444	1.00	-1.35	-0.12	1.31	3.13	2.06	5.71	1.36	8.43	0.90	cathepsin K; Cisk	X94444	cathepsin k precursor (ec 3.4.22.38).	cathepsin k (ec 3.4.22.38), encoded in the mouse by cisk, is implicated in bone resorption. expression is predominantly in osteoclasts; embryonic expression also takes place in some hypertrophic chondrocytes of growth cartilage	347.9 cM	Proteolytic	
M73748	1.00	-1.54	1.94	0.96	2.06	0.54	9.36	1.95	8.21	1.69	glycoprotein 38; Gp38	M73748	glycoprotein 38 precursor (gp38) (gts-8).			Cell Surface Protein	
X83601	1.00	1.04	0.95	1.04	1.89	3.72	14.68	1.06	8.18	2.71	pentaxin related gene; Ptx3	X83601	pentaxin-related protein ptx3 precursor (tumor necrosis factor-inducible protein tsg14).	a tnf stimulated gene. produced outside of the liver, increased levels of expression are induced by lps.	333.8 cM	Extracellular Protein	
X96639	1.00	-1.20	1.41	0.88	1.95	0.27	4.72	1.16	8.11	2.12	exostos (multiple 1; Ext1	X96639	exostosin-1 (putative tumor suppressor protein ext1) (multiple exostos protein 1).	appears to be a tumor suppressor.	1526.55 cM	Other	

C80103	1.00	-1.06	1.60	0.88	3.45	2.25	8.46	0.69	7.56	1.13	plastin 2, L, Pls2	C80103	I-plastin (lymphocyte cytosolic protein 1) (lep-1) (65 kda macrophage protein) (mp65)	actin-bundling protein.		Intracellular Protein	
M25324	1.00	1.00	1.80	0.68	1.26	0.26	6.55	1.35	7.55	2.74	selectin, lymphocyte; Sell	M25324	I-selectin precursor (lymph node homing receptor) (leukocyte adhesion molecule-1) (lam-1) (ly-22) (lymphocyte surface mel-14 endothelial cell adhesion molecule 1) (Lec-2) (Lec-2D)	cell surface adhesion protein. mediate the adherence of lymphocytes to endothelial cells of high endothelial venules in peripheral lymph nodes.	1 86.6 cM	Cell Surface Protein	
C80638	1.00	-1.07	0.91	0.65	1.97	0.69	7.94	3.14	7.51	1.81	EST, Unknown	C80638				EST; Unknown	
Msa.24575.0	1.00	1.03	0.77	0.72	2.95	0.34	6.02	0.16	7.13	1.48	EST	W82261				EST; Unknown	
Msa.1271.0	1.00	1.60	2.92	0.86	1.26	0.15	1.35	0.13	6.94	0.84	lactotransferrin; Ltf	J03298	lactotransferrin precursor (lactoferrin).	transferrins are iron binding transport proteins which can bind two atoms of ferric iron in association with the binding of an anion, usually bicarbonate.	9 61.0 cM	Intracellular Protein	
AA200615	1.00	-1.21	0.51	1.06	2.69	0.23	4.76	1.05	6.94	0.92	homologue of GENESEQN:Z36322 Mechanical stress induced cDNA encoding protein 608	AA200615		patent held by quark biotech, inc. - identification of stress induced genes for determining risk and preventing, treating or controlling osteoporosis		Other	
Msa.136.0	1.00	-1.02	1.05	0.73	2.34	1.16	4.34	0.20	6.84	1.15	interleukin 2 receptor, gamma chain; IL2rg	U21795	cytokine receptor common gamma chain precursor (gamma-c) (interleukin-2 receptor gamma chain) (il-2r gamma chain) (r664)	common subunit for the receptors for a variety of interleukins.	X 38.0 cM		

Msa.739.0	1.00	-1.82	-1.01	2.43	0.89	2.70	6.58	0.93	6.75	0.72	haptoglobin; Hp	M96827		haptoglobin combines with free plasma hemoglobin, preventing loss of iron through the kidneys and protecting the kidneys from damage by hemoglobin, while making the hemoglobin accessible to degradation	855.0 cM	Extracellular Protein	
D37837	1.00	1.26	1.48	0.88	2.18	0.80	5.85	1.31	6.34	1.47	plastin 2, L; Pls2	D37837	I-plastin (lymphocyte cytosolic protein 1) (lep-1) (65 kDa macrophage protein) (om65)	actin-binding protein.		Structural Protein	
UI7961	1.00	1.15	4.42	0.90	3.16	1.65	7.12	1.45	6.33	1.79	src associated in mitosis, 68 kDa; Sam68	UI7961					
U83903	1.00	-1.40	0.77	1.17	1.33	3.57	8.40	3.12	6.29	0.55	tumor necrosis factor induced protein 6; Tnfp6	U83903		induced in vitro in several cell types by proinflammatory cytokines, and in vivo in pathological conditions such as rheumatoid arthritis. interacts with link protein and aggrecan. involved in matrix dissociation and regulated by ph	2	Regulatory	
M59378	1.00	1.72	2.24	0.60	2.28	1.03	7.57	0.87	6.26	1.20	tumor necrosis factor receptor superfamily, member 1b; Tnfrsf1b	M59378	tumor necrosis factor receptor 2 precursor (tnfr2) (p75).	encodes the larger of two receptors for the tumor necrosis factor. its expression is regulated by external factors. a tnfrsf1b targeted null mutation shows normal t-cell development and activity, but is resistant to tnfr-induced cell death.	475.5 cM	Receptor	

U16985	1.00	1.02	1.86	0.93	1.83	0.19	5.30	0.24	6.23	1.04	lymphotoxin B; Ltb	U16985	lymphotoxin-beta (H beta) (tumor necrosis factor c).	member of the tnfr ligand family isolated from human t cells. only found on the cell surface, where it forms a 2:1 trimeric complex with lymphotoxin a. constitutively expressed in lymphoid and hematopoietic tissues, maximal in thymic medulla and splenic white pulp may play a specific role in immune response regulation. provides the membrane anchor for the attachment of the	17 19.06 cM	Cytokine	
Msa.1700.0	1.00	2.40	-0.32	0.82	2.12	3.77	5.59	2.04	5.93	0.88	phospholipase A2 group VII (platelet-activating factor acetylhydrolase, plasma); Pla2g7	U34277	platelet-activating factor acetylhydrolase precursor (ec 3.1.1.47) (paf acetylhydrolase) (paf 2-acylhydrolase) (dl- associated phospholipase a2) (dl-pla(2)) (2-acetyl-1-alkylglycerophosphocholine esterase) (1-alkyl-2-acetyl-glycerophosph	modulates the action of platelet-activating factor (paf) by hydrolyzing the sn-2 ester bond to yield the biologically inactive lyso-paf. has a specificity for substrates with a short residue at the sn-2 position. it is inactive against lo		Cytokine	
AA059883	1.00	-1.03	0.28	1.16	3.05	4.37	8.59	2.30	5.91	0.99	angiopoietin related	AA059883		the region of this genomic sequence that contains this sequence is listed as angiopoietin related.		Hemostasis	

U05837	1.00	-1.30	0.82	0.94	3.68	2.47	5.23	1.66	5.79	1.04	hexosaminidase A; Hexa	U05837	beta-hexosaminidase alpha chain precursor (ec 3.2.1.52) (n-acetyl- beta- glucosaminidase) (beta-n- acetylhexosaminida se) (hexosaminidase a).	lysosomal enzymes that contribute to the degradation of glycoproteins, glycolipids, and glycosaminoglycans. widely expressed, associated with ganglioside degradation. absence of the b form is associated with tau	9 29.0 cM	Proteolytic	
Msa.1600.0	1.00	1.12	-0.54	1.14	0.56	2.11	4.88	0.13	5.61	0.65	macrophage expressed gene 1; Mpeg1	L20315		transcripts from the gene are found at a high level in mature human and murine macrophages and at a moderate level in certain myelomonocytic cell lines		EST; Unknown	
L32974	1.00	-2.05	1.79	0.94	0.01	1.10	1.71	0.31	5.57	1.47	interferon-induced protein with tetratricopeptide repeats 3; Ifit3	L32974	interferon-induced protein with tetratricopeptide repeats 3 (ifit-3) (glucocorticoid- attenuated response gene 49 protein) (carta-49) (ira2)				
AA387033	1.00	1.17	1.46	0.66	2.73	1.63	5.21	0.80	5.54	0.46	Unknown	AA387033				EST; Unknown	
U72643	1.00	1.61	0.59	0.80	0.84	2.13	5.65	0.13	5.50	0.94	leucocyte specific transcript 1; Lst1	U72643		defense/immunity protein. an integral membrane protein.	17 19.06 cM	EST; Unknown	
AA174982	1.00	-1.02	1.24	0.85	3.75	2.69	5.03	1.76	5.39	0.63	coronin, actin binding protein 1A; Coro1a	AA174982	coronin-like protein p57 (coronin 1a) (fragment).	coronin participates in the remodelling of the cortical actin cytoskeleton that is responsible for phagocytosis and macropinocytosis. in mammalian neutrophils, a coronin- like protein is also associated with the	7 62.5 cM	Intracellular Protein	

U54984	1.00	-1.57	0.54	1.35	2.53	1.39	3.75	0.53	5.33	0.29	matrix metalloproteinase 14 (membrane-inserted); Mmp14	U54984	matrix metalloproteinase-14 precursor (ec 3.4.24.-) (mmp-14) (membrane-type matrix metalloproteinase 1) (mt-mmp 1) (mtmmp1).	expressed in invasive lung carcinoma cells, induces activation of gelatinase a on the cell surface and enhances cell invasion of basement membrane. specifically activates pro-gelatinase a. may trigger invasion by tumor cells by activation.	14 12.5 cM	Proteolytic		
L38281	1.00	-0.02	1.46	0.32	1.28	0.28	3.32	0.69	5.28	1.51	immune-responsive gene 1; Irg1	L38281	immune-responsive protein 1		14 53.5 cM			
AA245242	1.00	-1.73	1.18	0.56	2.72	1.42	4.17	0.72	5.23	0.51	MARCKS-like protein; Mlp	AA245242	cardiac (muscle) lim protein (cysteine-rich protein 3) (cyp3); marcks-related protein (marcks) (brain protein 52)	binds calmodulin and is a substrate for protein kinase c	4 59.0 cM	Signal Transduction		
AA183642	1.00	1.24	1.21	0.76	0.87	2.08	9.10	1.34	5.10	0.86	Unknown; EST	AA183642				EST; Unknown		
AA472322	1.00	1.00	3.10	0.52	2.32	1.32	6.68	0.28	5.09	1.40	EST; Unknown	AA472322				EST; Unknown		
X16133	1.00	-1.08	-0.57	1.49	-1.41	0.16	5.06	0.35	4.88	0.56	proteoglycan, secretory granule; Prg	X16133	secretory granule proteoglycan core protein precursor (mastocytoma proteoglycan core protein) (serglycin).	core protein for highly acidic proteoglycan containing glycosaminoglycan that are almost exclusively chondroitin sulfate c.		Intracellular Protein		
Msa.15534.0	1.00	-1.34	1.53	0.34	1.95	0.05	2.92	0.95	4.85	0.93	neutrophil cytosolic factor 2; Ncf2	W71124			1 76.1 cM			
Msa.22604.0	1.00	-1.06	-0.19	0.75	1.49	0.45	2.41	0.16	4.81	0.70		AA036297						
X61800	1.00	4.66	1.50	0.81	1.67	4.17	4.45	1.29	4.80	0.48	CCAAT/enhancer binding protein (C/EBP), delta; Cebpδ	X61800	ccat/enhancer binding protein delta (c/ebp delta) (c/ebp-related protein 3).	a transcription factor that binds to cis-regulatory dna sequences of viral genes and regulatory sequences of cellular genes that encode rna. important transcriptional activator in the regulation of genes involved in immune	16 9.0 cM	Transcription Factor		

AA408170	1.00	2.81	3.78	0.59	3.24	1.50	5.10	0.95	4.80	1.06	DEAD (aspartate-glutamate-alanine-aspartate) box polypeptide, Y chromosome; Dbv DNA segment, Chr 13, Abbott 1 expressed (TM7SF1)	AA408170			Y 2.07 cM	EST; Unknown	
C80550	1.00	-2.09	0.70	0.65	1.34	0.18	4.20	0.44	4.78	1.27	RAS-related C3 botulinum substrate 2; Rac2	C80550	ras-related c3 botulinum toxin substrate 2 (p21-rac2) (en-7 protein)	seven transmembrane domain protein, upregulated during kidney development.		Cell Surface Protein	
X53247	1.00	-1.36	0.91	0.62	0.75	1.80	3.63	0.14	4.77	0.85	RAS-related C3 botulinum substrate 2; Rac2	X53247	ras-related c3 botulinum toxin substrate 2 (p21-rac2) (en-7 protein)	murine homolog of a class of human ras-related proteins that are substrates for adenylation by botulinum toxin c3 adp-ribosyltransferase. expression is restricted to hematopoietic cells and organs. seems to be involved in the regulation of cell growth.		Signal Transduction	
M32370	1.00	-1.06	0.19	1.08	0.85	2.16	6.33	1.87	4.76	0.60	SFFV proviral integration 1; Sfp1	M32370	31 kda transforming protein (transcription factor pu.1).	encodes a tissue-specific binding protein, expressed in macrophages and b cells. media conditioned by erythroleukemia cells expressing sfp1 can promote proliferation of cell lines dependent on mcsf or gm-csf, may be inducing csf1 and csf2.	2 47.5 cM	Transcription Factor	
Msa.23838.0	1.00	-1.57	-1.50	1.20	0.38	3.42	3.77	0.52	4.66	1.00	tumor necrosis factor induced protein 6; Tnfp6	AA051341		induced in vitro in several cell types by proinflammatory cytokines, and in vivo in pathological conditions such as rheumatoid arthritis. interacts with link protein and aggregan. involved in matrix dissociation and regulated by phorbol esters.	2	Regulatory	

Msa.2530.0	1.00	1.00	1.00	1.30	0.30	1.23	0.23	5.83	1.26	4.66	1.14	vav oncogene; Vav	X64361	vav proto-oncogene.	probable exchange factor for a small ras-like gtp-binding protein. can be activated by truncation of the n-terminus.	17 32.7 cM	Signal Transduction
X07640	1.00	-1.80	1.45	0.57	0.02	1.79	4.71	1.02	4.65	0.90	integrin alpha M (Cd11b); Itgam	X07640	cell surface glycoprotein mac-1 alpha subunit precursor (cr-3 alpha chain) (cd11b) (leukocyte adhesion receptor mol) (integrin alpha m).	mac-1 is a cell surface glycoprotein of monocytes, macrophages and granulocytes which has been implicated in various adhesive interactions of these cells as well as in mediating the uptake of complement-coated particles. mac-1 is identical with cr-3, the receptor for the ic3b fragment of the third complement component. mac-1 probably recognize the	Cell Surface Protein		
Msa.641.0	1.00	-1.03	-0.19	1.41	1.05	2.42	4.35	0.06	4.63	0.84	Fc receptor, IgE, high affinity I, gamma polypeptide; Fcεr1g	W41745	high affinity immunoglobulin epsilon receptor gamma-subunit precursor (fcεr1) (ige fc receptor, gamma-subunit) (fc-ε-gamma-ri-gamma)	the gamma subunit has a critical role in allowing the ige fc receptor to reach the cell surface	1 93.3 cM	Receptor	
D10911	1.00	-1.22	1.65	0.35	2.18	1.00	4.95	0.08	4.59	0.99	a disintegrin and metalloprotease domain (ADAM) 8; Adam8	D10911	adam 8 precursor (ec 3.4.24.-) (a disintegrin and metalloproteinase domain 8) (cell surface antigen ms2) (macrophage cysteine-rich glycoprotein) (cd156-antigen)	possible involvement in extravasation of leukocytes.	7 F3-F5	Proteolytic	
X15591	1.00	1.53	0.39	0.89	0.63	1.86	3.57	0.27	4.58	0.64	cytotoxic T lymphocyte-associated protein 2 alpha; Ctla-2a	X15591	ctla-2-alpha protein precursor.	not known, expressed in activated t-cell.	13 36.0 cM	Cell Surface Protein	





Msa.2034.0	1.00	-1.02	0.25	0.81	1.38	2.45	5.16	0.29	4.46	0.72	CD53 antigen; Cd53	X97227	leukocyte surface antigen cd53 (cell surface glycoprotein cd53).	may be involved in growth regulation in hematopoietic cells.	3 50.5 cM	Cell Surface Protein	
AA103744	1.00	-1.31	1.73	1.20	3.98	2.12	7.13	2.86	4.42	0.81	ribosomal protein L27a; Rpl27a	AA103744	60S ribosomal protein L27a (l29).	plays cardinal role in calcium metabolism, and may be involved in neural transmission. buffers cytosolic calcium. may stimulate a membrane ca(2+)-atpase and a 3',5'-cyclic nucleotide phosphodiesterase. expressed in many tissues.	7 E2-F1	Metabolic	
AA189487	1.00	1.16	0.09	0.68	1.28	2.89	4.40	1.72	4.39	0.91	sushi-repeat-containing protein, X chromosome; Spx-pending	AA189487				EST; Unknown	
Msa.1843.0	1.00	-1.25	0.33	0.73	0.53	1.90	5.85	0.19	4.32	1.17	chemokine (C-C) receptor 1, chemokine (C-C) receptor 1-like 2; Cmkbr1, Cmkbr12	U28404	c-c chemokine receptor type 1 (c-c ckr-1) (cc-ckr-1) (ccr-1) (cckr1) (macrophage inflammatory protein-1 alpha receptor) (mip-1alpha-r) (ranies-1alpha-r), probable c-c chemokine receptor type 3 (c-c ckr-3) (cc-ckr-3) (ccr-3) (cckr3) (macrophage inflammatory protein-1 alpha receptor-like 2)	mip-1a-receptor. all three of the cmkbr1 genes has been found in leukocytes, but their patterns of expression differ in solid organs. cmkbr1 is expressed in heart, spleen, and lung;	9 72.0 cM	Receptor	
Msa.31660.0	1.00	-1.04	0.86	0.72	0.81	2.03	4.38	0.48	4.28	0.73	CD53 antigen; Cd53	AA105582	leukocyte surface antigen cd53 (cell surface glycoprotein cd53).	may be involved in growth regulation in hematopoietic cells.	3 50.5 cM	Cell Surface Protein	
U29947	1.00	-1.41	-2.19	1.91	3.44	5.25	7.01	4.87	4.27	1.44	mannosidase 2, alpha B1; Man2b1	U29947	lysosomal alpha-mannosidase precursor (ec 3.2.1.24) (mannosidase, alpha b) (lysosomal acid alpha-mannosidase) (laman)	necessary for the catabolism of n-linked carbohydrates released during glycoprotein turnover. cleaves all known types of alpha-mannosidic linkages.	8 37.0 cM	Regulatory	

AA546670	1.00	-2.14	0.74	0.79	2.40	1.24	3.20	0.63	4.20	0.32	myristoylated alanine rich protein kinase C substrate; Macs	AA546670	myristoylated alanine-rich c-kinase substrate (marks).	marks is the most prominent cellular substrate for protein kinase c. this protein binds calmodulin, actin, and synapsin. marks is a filamentous (f) actin cross-linking protein	10 22.0 cM		
Msa.40979.0	1.00	-1.35	2.97	0.90	1.29	2.51	3.55	1.17	4.19	1.07		AA161769					
AA544540	1.00	-1.10	2.67	0.86	2.10	1.04	4.47	1.05	4.18	0.85		AA544540					
Msa.1099.0	1.00	1.13	0.92	0.61	2.24	0.74	3.25	0.27	4.15	0.40	neuron specific gene family member 1; Nsg1	W46015	neuron specific protein family member 1 (brain neuron cytoplasmic protein 1) (p21) (m234)		5 21.0 cM	EST; Unknown	
U36993	1.00	1.03	0.47	0.64	0.33	1.42	4.96	1.07	4.12	0.97	cytochrome P450, 7b1; Cyp7b1	U36993	heme-containing enzymes involved in metabolism of a number of endogenous substrates. expressed principally in brain, only low levels found in liver. most closely resembles p45vii a1, cholesterol 7 a hydroxylase, but cleaves cholesterol from it		3 1.0 cM	Metabolic	
AA170444	1.00	1.16	1 10	0.52	1.15	0.07	2.61	0.32	4.04	0.68	EST; Unknown	AA170444				EST; Unknown	
AA289661	1.00	-1.32	0.82	0.90	1.52	2.69	4.34	0.86	4.01	0.60	EST; Unknown	AA289661				EST; Unknown	
K01496	1.00	-1.66	0.56	0.76	1.77	3.25	4.14	1.13	4.01	0.40	histocompatibility 2, complement component factor B; H2-Bf	K01496	complement factor b precursor (ec 3.4.21.47) (c3/c5 convertase).	factor b which is part of the alternate pathway of the complement system is cleaved by factor d into 2 fragments: ba and bb. bb, a serine protease, then combines with complement factor 3b to generate the c3 or c5 convertase	17 18.85 cM	Hemostasis	

AA189758	Wbser5 gene product; Wbser5	AA189758	0.32	4.00	0.42	5.25	1.23	2.27	0.52	1.44	-1.21	1.00	(see note) contains two lim domains and a putative protein kinase domain. high expression levels in CNS, particularly in spinal cord, cranial nerve and dorsal root ganglia. lesser expression in heart and skeletal muscle. may be a component of		Regulatory
U88328	cytokine inducible SH2-containing protein 3 (SOCS3); Cish3	U88328	0.28	4.00	1.50	5.37	4.32	1.95	0.87	0.18	1.73	1.00	socs-1 inhibits the differentiation of m1 cells in response to il-6. transcription of all four socs genes is increased rapidly in response to il-6, in vitro and in vivo, suggesting they may act in a classic	ECM (Matrix Prot)	
AA015322	SPARC-related protein (SRG) (related to osteonectin)	AA015322	1.02	3.98	2.87	2.86	2.09	-0.73	0.77	-1.39	1.70	1.00	nascent feedback		Other
M13963	guanine nucleotide binding protein, alpha inhibiting 2; Gna12	M13963	0.80	3.92	1.35	3.64	0.25	1.70	0.75	2.19	-1.39	1.00	the g(i) proteins are involved in hormonal regulation of adenylate cyclase; they inhibit the cyclase in response to beta- adrenergic stimuli	9 59.0 cM	Signal Transduction
Z16078	CD53 antigen; Cd53	Z16078	0.55	3.92	0.16	3.64	2.18	0.83	1.04	0.06	1.06	1.00	may be involved in growth regulation in hematopoietic cells.	3 50.5 cM	Cell Surface Protein
M63836	beta-glucuronidase structural; Gus-s	M63836	0.12	3.87	0.75	3.88	2.02	0.65	0.81	-0.08	-1.50	1.00	aka gusb	5 72.0 cM	Metabolic
D11468	immunoglobulin alpha heavy chain DNA segment, Chr X, Immunex 39, expressed;	D11468	1.15	3.84	1.00	0.95	0.93	2.26	0.78	1.20	1.82	1.00			Extracellular Protein
AA266385		AA266385	0.84	3.84	0.46	3.88	0.04	1.12	0.58	1.00	-1.03	1.00		X 1.6 cM	EST; Unknown

Gene	1.00	3.11	2.20	1.45	5.23	2.30	3.07	1.90	3.83	1.07	D site albumin promoter binding protein, Dbp	U29762	d-site-binding protein (albumin d box-binding protein).	this transcriptional activator recognizes and binds to the sequence 5'-rtttaggaay-3' found in the promoter of genes such as albumin, cyp2a4 and cyp2a5. it is not essential for circadian rhythm generation, but modulates important clock output genes. may be a direct target for regulation by the circadian pacemaker component clock. may affect circadian period	7 23.0 cM	Transcription Factor
U29762	1.00	1.34	0.21	0.82	0.49	2.05	4.56	0.86	3.82	0.51	EST; Unknown	AA177433				EST; Unknown
D28599	1.00	-1.28	0.91	0.59	1.18	0.13	4.59	0.54	3.81	0.96	chondroitin sulfate proteoglycan 2; Cspg2	D28599	versican core protein precursor (large fibroblast proteoglycan) (chondroitin sulfate proteoglycan core protein.2) (nc-m)	extracellular matrix link protein.	13 55.0 cM	ECM (Matrix Prot)
D50494	1.00	-2.14	11.79	6.74	3.21	2.21	4.11	1.50	3.78	0.92	DEAD (aspartate-glutamate-alanine-aspartate) box polypeptide 6; Ddx6	D50494	probable atp-dependent rna helicase p54 (oncogene rck homolog) (dead-box protein.6)		9 26.0 cM	
L15443	1.00	1.18	0.10	1.49	2.42	0.90	3.03	0.39	3.78	0.42	membrane component, surface marker 1; M3s1	L15443				Cell Surface Protein
ET62103	1.00	-1.46	10.80	4.19	6.12	8.71	6.88	5.42	3.78	2.72	apoptosis inhibitor 1; bire2 (Api1)	ET62103	inhibitor of apoptosis protein 1 (miap1) (miap-1).	traf1 and/or traf2 associated protein of the rap (inhibitor of apoptosis) family. iaps may play a role in tumour progression rather than tumour initiation, making the iaps an attractive therapeutic target	9 A2	Regulatory
U88908	1.00	1.55	1.04	0.58	1.90	0.66	5.13	1.33	3.77	0.55		U88908				

AA020512	1.00	1.01	1.31	0.45	1.33	0.02	3.97	0.39	3.75	0.87	caspase 6; Casp6	AA020512	caspase-6 precursor (ec 3.4.22.-) (apoptotic protease mch-2).	involved in the activation cascade of caspases responsible for apoptosis execution. cleaves poly(adp-ribose) polymerase in vitro, as well as lamins. overexpression promotes programmed cell death (by caspase-6).			
AA172851	1.00	-1.04	0.26	0.77	0.44	1.66	4.53	0.34	3.75	0.58	EST; Unknown	AA172851		no match on blast	EST; Unknown		
X75926	1.00	2.26	0.55	0.56	1.93	0.81	2.51	0.07	3.74	0.54	ATP-binding cassette, sub-family A (ABC1), member 1; Abca1	X75926	atp-binding cassette, sub-family a, member 1 (atp-binding cassette transporter 1) (atp-binding cassette 1) (abc-1)	camp-dependent and sulfonylurea-sensitive anion transporter. key gatekeeper influencing intracellular cholesterol transport (for similarity)	4 23.1 cM		
Msa.22134.0	1.00	-1.17	-0.52	1.02	2.09	0.87	3.68	0.40	3.72	0.48	Unknown	AA031158			EST; Unknown		
U59463	1.00	1.12	1.47	0.50	1.56	0.11	3.86	0.75	3.72	0.86	caspase 11; Casp11	U59463	caspase-11 precursor (ec 3.4.22.-) (ich-3 protease).	involved in the activation cascade of caspases responsible for apoptosis execution. promotes il-1 beta processing by ice, so may also have a role in inflammatory responses			
Msa.510.0	1.00	-2.49	-0.90	1.04	0.25	1.81	2.97	0.16	3.71	0.50	histocompatibility 2, complement component factor B; H2-Bf	M57890	complement factor b precursor (ec 3.4.21.47) (c3/c5 convertase).	involved in the alternative or properdin complement pathway	17 18.85 cM	Hemostasis	
AA172673	1.00	1.32	1.17	0.44	1.53	0.29	3.48	0.41	3.70	0.63	paternally expressed gene 3; Peg3	AA172673			7 6.5 cM	EST; Unknown	
AA051505	1.00	-2.70	-1.31	0.66	0.87	2.64	3.03	0.83	3.70	0.72	EST; unknown	AA051505			EST; Unknown		
U89269	1.00	-1.43	0.80	0.75	2.05	3.22	4.88	1.64	3.69	0.60	cathepsin C; Cisc	U89269	dipeptidyl-peptidase i precursor (ec 3.4.14.1) (dpp-i) (dppi) (cathepsin c) (cathepsin j) (dipeptidyl transferase).	mammalian lysosomal cysteine proteinases. plays a role in protein catabolism within the cell, and may be involved in tumor metastasis. expression is widely distributed, with some variability in level, in mouse tissues	7 D3-E1.1	Proteolytic	

J03535	1.00	-1.00	0.79	0.72	2.43	1.30	3.93	1.01	3.68	0.20	embigin; Emb	J03535	pou domain, class 6, transcription factor 1 (octamer-binding transcription factor emb) (transcription regulatory protein mcp-1), teratocarcinoma glycoprotein gp-70 precursor.	embigin and basigin are highly glycosylated glycoproteins with two immunoglobulin domains and form a subgroup in the immunoglobulin superfamily. embigin is strongly expressed in the endoderm	15 57.0 cM	Transcription Factor	
AA592768	1.00	1.54	2.46	0.83	4.64	1.76	5.53	2.15	3.66	0.49	small proline-rich protein 2A; Spr2a	AA592768		small proline-rich (spr) proteins are structural components of the cornified cell envelope of stratified squamous epithelia, they are subdivided into three families, i.e., spr1, spr2, and spr3, of which the spr2 family is the most	3 45.2 cM	Structural Protein	
AA259937	1.00	-5.79	-1.14	0.85	0.60	2.69	2.67	0.61	3.65	0.51	procollagen, type III, alpha 1; Col3a1	AA259937	collagen alpha 1 (iii) chain precursor.	collagen type iii occurs in most soft connective tissues along with type I	1 21.1 cM	ECM (Matrix Prot)	
M31419	1.00	1.09	1.63	0.64	1.42	0.20	4.04	0.65	3.65	1.09	interferon activated gene 204; Ifi204	M31419	interferon-activatable protein 204 (ifi-204) (interferon-inducible protein)	member of a cluster of genes activated by interferon on chr 1. function unknown.	1 95.2 cM	Unknown	
X13333	1.00	-1.22	-0.21	0.70	0.54	1.83	3.09	0.31	3.65	0.66	CD14 antigen; Cd14	X13333	monocyte differentiation antigen cd14 precursor (lps-r) (myeloid cell-specific leucine-rich glycoprotein).	a cell surface marker of human monocytes and macrophages. serves as an lps receptor controlling cell activation under physiological conditions. when lps binds to cd14 the cells become activated and release cytokines and inhibit cell surface	18 31.0 cM	Cell Surface Protein	
Msa.17760.0	1.00	1.18	-0.09	0.59	1.30	0.26	2.25	0.17	3.65	0.46		W98059					
Msa.10687.0	1.00	-7.85	-1.32	1.27	0.53	1.55	2.43	0.50	3.62	0.29	Unknown	W48936				EST; Unknown	

\* \* \*

Gene	1.00	-2.89	-2.10	0.78	-0.63	1.88	1.84	0.27	3.59	0.99	mesoderm specific transcript; Mest	D16262	aka pgl-1 — the mouse pgl-1 gene is an imprinted gene that is expressed particularly in mesodermal tissues in early embryonic stages	6.7.5 cM	Cytokine	
M31131	1.00	-1.13	0.01	0.80	0.44	1.57	2.15	0.39	3.58	0.51	cadherin 2; Cdh2	M31131	neural-cadherin precursor (n-cadherin).	18.6.0 cM	Cell Surface Protein	
AA161790	1.00	-1.89	2.16	0.67	2.68	0.16	3.54	0.34	3.56	0.25	aplysia ras-related homolog A2; Arha2	AA161790	regulates a signal transduction pathway linking plasma membrane receptors to the assembly of focal adhesions and actin stress fibers.	2.37.0 cM	Intracellular Protein	
D83266	1.00	-1.47	0.12	0.69	0.47	1.66	4.05	0.84	3.55	0.78	vav oncogene; Vav	D83266	vav proto-oncogene; binds to grb2 and grb3.	17.32.7 cM	Signal Transduction	*
M35833	1.00	-1.98	-1.06	0.88	0.24	1.52	0.75	0.95	3.54	0.48	midkine; Mdk	M35833	midkine (mk) is a heparin-binding growth/differentiation factor implicated in the control of development and repair of various tissues. mk plays important roles in chondrogenesis and contributes to bone.	2.53.0 cM	Cytokine	*



Accession	1.00	-1.89	-2.21	1.27	0.70	2.36	2.59	0.70	3.54	0.51	Integrin binding sialoprotein; lbsp	L23801	bone sialoprotein ii precursor (bsp ii) (cell-binding sialoprotein) (integrin-binding sialoprotein).	aka integrin binding sialoprotein -- bone sialoprotein (bsp) is a small, highly posttranslationally modified integrin binding protein found in the mineral compartment of developing bone. contains a conserved arg-gly-asn (rgd) integrin-binding site.	556.0 cM	ECM (Matrix Prot)	
U78818	1.00	-2.25	1.14	0.45	0.37	0.02	3.63	0.37	3.54	0.45	downstream of tyrosine kinase 1; Dok1	U78818			634.73 cM		
U19482	1.00	-1.31	1.07	0.85	0.87	2.68	6.02	0.87	3.52	0.32	small inducible cytokine A9; Scya9	U19482	small inducible cytokine a9 precursor (macrophage inflammatory protein 1-gamma) (mip-1-gamma) (macrophage inflammatory protein-related protein-2) (mip-2) (ccf18).	a.k.a mip-1 gamma or ccf18 -- chemokines play an important role in immune and inflammatory responses by inducing migration and adhesion of leukocytes. ccf18 mma is constitutively expressed in macrophage and monocyte-derived cells.	1147.4 cM	Cytokine	
U21795	1.00	-1.16	1.05	0.42	0.56	0.36	4.01	0.56	3.51	0.61	interleukin 2 receptor, gamma chain; IL2rg	U21795	cytokine receptor common gamma chain precursor (gamma-c) (interleukin-2 receptor gamma chain) (il-2r gamma chain) (c64).	common subunit for the receptors for a variety of interleukins.	X38.0 cM		
M27960	1.00	-1.14	-0.88	1.09	0.51	2.91	5.45	0.51	3.49	0.49	interleukin 4 receptor, alpha, IL4ra	M27960	interleukin-4 receptor alpha chain precursor (il-4r-alpha).	a receptor for il4, a mediator of the th2 (b cell) response. acts as an antagonist to il4, presumably by adsorbing il4 molecules.	762.0 cM	Receptor	
W11156	1.00	0.01	0.61	1.10	0.05	0.10	3.19	0.05	3.49	0.67	EST; unknown	W11156		some similarity to j399 human gamma-interferon-inducible protein		EST; Unknown	



72



U29539	1.00	-1.52	0.42	0.73	1.06	2.21	3.37	0.68	3.25	0.38	lysosomal-associated protein transmembrane 5; Laptm5	U29539	lysosomal-associated protein (retinoic acid- inducible e3 protein).	the expression pattern of the gene together with preliminary evidence that the protein interacts with ubiquitin indicates that the protein may have a special functional role during embryogenesis and in adult hematopoietic cells. it			Proteolytic	
AA125580	1.00	-1.07	1.43	0.44	1.46	0.06	3.65	0.56	3.22	0.64	synaptosomal-associated protein, 23kD; Snap23	AA125580			2 61.8 cM			
X93328	1.00	-1.75	0.32	0.79	0.38	1.69	3.03	0.17	3.21	0.44	EGF-like module containing, mucin-like, hormone receptor-like sequence 1; Emr1	X93328	cell surface glycoprotein emr1 precursor (emr1 hormone receptor) (cell surface glycoprotein f4/80)	probably involved in cell adhesion within tissues and receptor signalling.	17 34.3 cM	Cell Surface Protein		
Msa.35983.0	1.00	-1.10	-1.46	1.04	0.12	1.54	2.65	0.50	3.19	0.26	secreted phosphoprotein 1; Spp1	AA123395	precursor (bone sialoprotein 1) (early t lymphocyte activation 1 protein) (secreted phosphoprotein 1) (spp-1) (Zar) (calcium oxalate crystal growth inhibitor associated)	binds tightly to hydroxyapatite. appears to form an integral part of the mineralized matrix. probably important to cell-matrix interaction.	5 56.0 cM	Cytokine		*
Msa.2173.0	1.00	1.16	0.76	0.57	0.37	1.73	3.13	0.44	3.17	0.38	inhibin beta-A; Inhba	X69619	inhibin beta a chain precursor (activin beta-a chain).	inhibin is a gonadal glycopeptide that inhibits the secretion of follitropin by the pituitary gland. on the other hand activin activates the secretion of follitropin. activin is also important in embryonic axial development	13 10.0 cM	Cytokine		*

AF004874	1.00	-1.80	-0.96	0.71	0.93	2.54	3.03	1.07	3.16	0.29	latent transforming growth factor beta binding protein 2; Lbp2	AF004874	human protein is structurally similar to fibrillin. plays a role in bone biology? lbp-2 gene expression in mouse embryos was restricted to cartilage perichondrium and blood vessels, a somewhat surprising result since other lbp genes are expressed in other tissues.	12 D	Unknown	
L38971	1.00	-2.23	-1.09	0.80	1.13	2.99	0.72	1.31	3.15	0.99	integral membrane protein 2; ltm2	L38971	integral membrane protein 2a (e25 protein).	X 37.0 cM		
Msa.64.0	1.00	-1.16	0.10	0.84	0.73	1.75	3.06	0.40	3.15	0.40	collagen binding protein 1; Cbp1	D12907	47 kda heat shock protein precursor (collagen-binding protein 1) (serine protease inhibitor if6)		Intracellular Protein	
M31418	1.00	-1.10	1.14	0.90	1.73	2.88	3.24	0.81	3.13	0.18	interferon activated gene 202A,interferon activated gene 202B; Ifi202a,Ifi202b	M31418	interferon-activatable protein 202a (ifi-202a) (interferon-inducible protein p202a).interferon-activatable protein 202b (ifi-202b) (interferon-inducible protein p202b).	1,1 95.2 cM		
AA177300	1.00	-1.63	-1.28	0.98	0.84	2.56	3.22	1.35	3.11	0.45	DNA segment, Chr 13, Abbott 1 expressed; D13Abble	AA177300	seven transmembrane domain protein, upregulated during kidney development.	13 6.0 cM	Cell Surface Protein	
X56304	1.00	-1.02	-2.37	1.63	0.48	2.28	2.63	0.39	3.10	0.34	tenascin C; Tnc	X56304	glycoprotein expressed in developing brain, mesenchyme, and cartilage, osteoblasts, periosteal and perichondrial cells, and articular surfaces, and is maintained into adult stages in some tissues. notably, the	4 32.2 cM	ECM (Matrix Prot)	

U05265		1.00	-1.14	0.38	0.61	0.20	1.56	4.01	0.57	3.06	0.66	glycoprotein 49 B; Gp49b	U05265	mast cell surface glycoprotein gp49a precursor, mast cell surface glycoprotein gp49b precursor.	preferentially expressed on mouse interleukin-3-dependent, bone marrow-derived mast cells, which are immature progenitor cells. members of the protein family are alternative splices of <i>cd49a-cd49i</i> .	10 32.0 cM	Cell Surface Protein	
D12907		1.00	-1.56	0.04	0.74	0.80	1.99	2.84	0.37	3.03	0.15	collagen binding protein 1; Cbp1	D12907	47 kda heat shock protein precursor (collagen-binding protein 1) (serine protease inhibitor 16).	binds specifically to collagen. could be involved as a chaperone in the biosynthetic pathway of collagen.		Intracellular Protein	
D86422		1.00	7.64	1.04	1.06	7.03	8.15	0.24	1.30	3.03	1.86	keratin-associated protein 8-2; Krtap8-2	D86422					
V00802		1.00	3.13	1.02	0.89	2.20	0.79	0.74	0.96	3.02	0.42		V00802				EST; Unknown	
AA408463		1.00	1.15	-0.68	0.55	0.66	2.06	2.37	0.79	3.02	0.25	probable match to cadherin 5	AA408463		vasculo-endothelial (ve)-cadherin is specifically expressed in endothelial cells. expressed in ubiquitously in vascular structures. cadherins act as cell adhesion receptors		Cell Surface Protein	
U52524		1.00	-1.35	0.32	0.62	0.41	1.81	3.16	0.79	3.00	0.56	hyaluronan synthase 2; Has2	U52524	hyaluronan synthase 2 (ec 2.4.1.-) (hyaluronate synthase 2) (hyaluronic acid synthase 2) (ha synthase 2)	play a role in hyaluronan/hyaluronic acid (ha) synthesis.	15 31.2 cM	Other	
X14951		1.00	-1.02	0.33	0.69	0.52	2.07	2.90	0.25	2.99	0.46	integrin beta 2 (Cd18); Itgb2	X14951	cell surface adhesion glycoproteins lfa-1/cr3/p150,95 beta-subunit precursor (integrin beta-2) (cd18 antigen) (complement receptor c3 beta-1 component)	associates with alpha-1 (lfa-1) to interact with icam-1, and with alpha-m (mac-1) or alpha-x to form the receptor for the ic3b fragment of the third complement component	10 41.5 cM	Cell Surface Protein	

AA537404	1.00	-1.18	-0.66	0.85	0.43	1.49	2.74	0.44	2.97	0.34	thymosin beta-10; from rat	AA537404	expressed at relatively high levels in embryonic tissues, and its mRNA is abundant in a variety of tumors and tumor cell lines. a major intracellular g-actin binding protein. (a) plays a significant and possibly obligatory role in cell division.		Structural Protein	
AA285635	1.00	2.08	-0.32	0.77	3.37	2.34	3.01	1.30	2.95	0.72	ectoplacental cone, invasive trophoblast giant cells, extraembryonic ectoderm and chorion sequence 21; Epc21-encoding	AA285635			EST; Unknown	
Msa.8157.0	1.00	-1.28	-0.93	0.86	0.17	1.94	2.89	0.07	2.95	0.33	cathepsin S; Cts	AA089333	the cathepsins are mammalian lysosomal cysteine proteinases. they play an important role in protein catabolism within the cell, and may be involved in tumor metastasis	3 42.7 cM	Proteolytic	
D50586	1.00	1.00	0.03	0.57	0.22	1.43	3.12	0.85	2.95	0.33	tissue factor pathway inhibitor 2; Tfi2	D50586		6 1.0 cM		
M74149	1.00	-1.31	-1.11	1.25	0.64	1.77	2.40	0.75	2.94	0.38	creatine kinase, brain; Ckb	M74149	reversibly catalyzes the transfer of phosphate between atp and various phosphogens (e.g. creatine phosphate). creatine kinase isoenzymes play a central role in energy transduction in tissues with large, fluctuating energy demands, such as skeletal muscle, heart, brain, and	12 55.0 cM	Metabolic	



Msa.805.0	1.00	1.60	2.03	1.10	2.06	0.82	1.55	0.25	2.94	1.18	immunoglobulin heavy chain 1 (serum IgG2a); immunoglobulin heavy chain 3 (serum IgG2b); immunoglobulin heavy chain 4 (serum IgG1); immunoglobulin heavy chain 6 (heavy chain of IgM); IgH-1, IgH-3, IgH-4, IgH-5	J00475				12 58.0 cM	Hemostasis	
Msa.7614.0	1.00	-1.36	-0.23	0.68	0.48	1.57	4.41	0.21	2.93	0.49	homolog (84%) of human beta-tubulin	W18778					EST; Unknown	
Msa.3176.0	1.00	1.60	0.10	0.64	1.34	0.17	1.78	0.17	2.91	0.37	cathepsin E; Cse	X97399	cathepsin E precursor (ec 3.4.23.34).	due to its intracellular location and distribution in lymphoid associated tissue, it may have a role in immune function		1 69.1 cM	Proteolytic	
X60367-2	1.00	1.25	-0.64	0.89	1.48	0.40	1.75	0.34	2.91	0.22	retinol binding protein 1, cellular; Rbp1	X60367	retinol-binding protein i, cellular (mrbp).	the rbp1 gene encodes crbp, a protein present in a wide variety of adult rat tissues but most abundant in liver and kidney.		9 52.0 cM	Regulatory	
AA542220	1.00	1.33	0.43	1.01	2.01	3.11	3.69	1.55	2.90	0.77	TBX1 protein; TBX1	AA542220	tbx1 protein (t-box protein 1) (testis-specific t-box protein) (fragment).	estrogen treatment resulted in a rapid and transient increase in ect-1 messenger rna; steady state levels peaked between 2-3 h, returning to basal levels by 6 h. this increase was not abolished by pretreatment with cycloheximide, induction.			Intracellular Protein	
ab000822	1.00	1.09	1.15	0.61	2.65	1.54	3.02	0.68	2.90	0.52	synaptosomal-associated protein, 23kD; Snap23	AB000822				2 61.8 cM		
ab009287	1.00	-1.10	-0.70	0.66	0.26	1.71	2.69	0.03	2.89	0.42	CD68 antigen; Cd68	AB009287	macrosialin precursor (cd68 antigen).	a.k.a. macrosialin --the glycoprotein macrosialin is expressed specifically in murine monocytes and macrophages.		11 39.0 cM	Cell Surface Protein	

M74227	1.00	-1.62	-1.17	0.88	0.50	1.83	1.58	0.28	2.88	0.15	peptidylprolyl isomerase C; Ppic	M74227	peptidyl-prolyl cis-trans isomerase c (ec 5.2.1.8) (ppase) (rotamase)	ppases accelerate the folding of proteins.		Intracellular Protein	
Msa.1629.0	1.00	1.00	0.48	1.03	0.32	1.52	2.16	0.22	2.88	0.26	proteasome (prosome, macropain) subunit, beta type 8 (large multifunctional protease 7); Pmb8	U22031	proteasome component c13 precursor (ec 3.4.99.46) (macropain subunit c13) (multicatalytic endopeptidase complex subunit c13).	the proteasome is a multicatalytic proteinase complex which is characterized by its ability to cleave peptides with arg, phe, tyr, leu, and glu adjacent to the leaving group at neutral or slightly basic ph. the proteasome has an atp-dependent proteolytic activity. this subunit may be involved in	17 18.61 cM	Proteolytic	
X04648	1.00	1.05	-0.62	0.83	0.26	2.21	3.17	0.23	2.87	0.37	Fc receptor, IgG, low affinity IIb; Fcgr2b	X04648	low affinity immunoglobulin gamma fc region receptor ii precursor (fc- gamma rii) (fcrr) (igg fc receptor ii beta) (fc gamma receptor ii) (fcgammariib).	a second low affinity receptor for the fc portion of igg. fc\gammarii and fc\gammarii receptors are identical to low affinity receptor for igg on mouse mast cells and macrophages. fc\gammarii is immunologically	1 92.3 cM	Receptor	
M64086	1.00	-1.36	-3.46	4.25	1.63	3.55	4.80	1.51	2.87	0.36	serine protease inhibitor 2-2; Spi2-2	M64086				Proteolytic	
Msa.27449.0	1.00	1.12	-1.53	0.84	0.19	1.58	2.12	0.37	2.87	0.09	secreted phosphoprotein 1; Spp1	AA066782	osteopontin precursor (bone sialoprotein 1) (minopontin) (early t lymphocyte activation 1 protein) (secreted phosphoprotein 1) (spp-1) (2ar) (calcium oxalate crystal growth inhibitor protein)	binds tightly to hydroxyapatite. appears to form an integral part of the mineralized matrix. probably important to cell-matrix interaction.	5 56.0 cM	ECM (Matrix Prot)	
AA140446	1.00	-1.61	-1.09	0.72	0.32	1.85	4.28	2.43	2.84	0.37	DNA segment, Chr 13, Abbott 1 expressed; D13Abble	AA140446		seven transmembrane domain protein, upregulated during kidney development.	13 6.0 cM	Cell Surface Protein	

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AA547057	1.00	1.21	1.69	0.71	1.88	0.13	3.69	0.54	2.83	0.29	ets variant gene 6 (TEL oncogene); ETV6	AA547057	ets-related protein tel (ets translocation variant 6).		663.9 cM	Extracellular Protein	
AA259726	1.00	1.02	0.74	0.62	2.33	1.10	3.74	1.63	2.82	0.44	EST; Unknown	AA259726				EST; Unknown	
ET61206	1.00	2.05	1.11	0.76	1.81	0.45	0.70	1.08	2.81	0.31		ET61206				EST; Unknown	
Msa.10497.0	1.00	-4.02	2.16	0.97	0.52	2.77	3.48	2.46	2.79	1.43		W48224					
ET62056	1.00	2.54	-0.61	1.70	1.79	0.33	0.68	1.04	2.78	0.40	immunoglobulin rearranged kappa chain	ET62056				Extracellular Protein	
L06039	1.00	-1.13	0.20	0.74	0.84	2.13	2.78	1.03	2.77	0.13	platelet/endothelial cell adhesion molecule; Pecam	L06039	platelet endothelial cell adhesion molecule precursor (pecam-1) (cd31 antigen).	functions in cell-cell adhesion...expression in lymphocytes transmigration the endothelial cell lining...the function of pecam in the emigration process is not solely to bring leukocytes into contact with the vascular endothelium	631.5 cM	Hemostasis	
U90355	1.00	-1.22	-1.48	1.29	0.21	1.62	2.12	0.27	2.77	0.25	fascin homolog 1 (actin bundling protein, Strongylocentrotus purpuratus); Fscn1	U90355	fascin.	organizes filamentous actin into bundles with a minimum of 4:1:1 actin/fascin ratio.	586.0 cM	Structural Protein	
AA255186	1.00	-1.71	0.71	0.70	0.32	2.47	3.26	0.66	2.76	0.24	cathepsin S; Cts	AA255186		lysosomal cysteine proteinase	342.7 cM	Proteolytic	
AA030649	1.00	-1.29	-0.57	0.54	0.18	2.27	1.99	0.28	2.76	0.51	procollagen, type V, alpha 1; Col5a1	AA030649		type v collagen is a member of group i collagen (fibrillar forming collagen). collagen v is expressed in connective tissue in close contact with the vascular basement membrane in bone, skin, cartilage, tendon, bone marrow stromal cells.	218.0 cM	ECM (Matrix Prot)	
Msa.544.0	1.00	-2.55	-3.78	2.77	-0.05	1.74	1.98	0.15	2.75	0.27	procollagen, type V, alpha 2; Col5a2	L02918				ECM (Matrix Prot)	
AA690738	1.00	-1.06	0.68	0.56	1.54	0.10	2.40	0.32	2.74	0.47	EST; Unknown	AA690738				EST; Unknown	
AA711271	1.00	-1.70	-0.60	0.75	0.81	2.07	3.05	1.23	2.73	0.39	EST; Unknown	AA711271				EST; Unknown	

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L39017	1.00	-1.55	1.61	0.77	1.47	2.56	1.52	1.35	2.72	0.46	protein C receptor, endothelial; Procr	L39017	dipeptidyl-peptidase i precursor (ec 3.4.14.1) (dpp-i) (dppi) (cathepsin c) (cathepsin j) (dipeptidyl transferase).	the cathepsins are mammalian lysosomal cysteine proteases. they play an important role in protein catabolism within the cell, and may be involved in tumor metastasis.	2 H1-3		
Msa.38948.0	1.00	-1.30	-1.35	1.58	0.59	1.88	3.06	0.72	2.69	0.38	cathepsin C; Cisc	AA144887			7 D3-E1.1	Proteolytic	
AA184116	1.00	1.05	0.26	0.59	0.78	1.84	2.56	0.58	2.65	0.34	homolog of Alpha-actinin (human)	AA184116		function: facin cross-linking protein which is thought to anchor actin to a variety of intracellular structures. this is a bundling protein. likely involved in wnt binding and signal transduction, deleted in breast carcinomas		Structural Protein	
U88566	1.00	-1.29	-1.69	1.36	0.35	2.47	3.39	0.76	2.64	0.25	secreted frizzled-related sequence protein 1; Sfrp1	U88566			8 9.5 cM	Cytokine	
AA475191	1.00	-1.11	1.12	0.68	2.10	0.47	3.44	0.86	2.64	0.25	cyclin-dependent kinase regulatory subunit 1; Cks1	AA475191				Signal Transduction	
ET61664	1.00	-1.03	-0.49	1.06	0.19	1.69	2.98	0.11	2.63	0.42	Fc receptor, IgG, low affinity IIb; Fcgr2b	ET61664	low affinity immunoglobulin gamma fc region receptor ii precursor (fc-gamma rii) (fcrii) (igg fc receptor ii beta) (fc gamma receptor iib) (fcgammariiib).	is a receptor for the fc region of complexed immunoglobulins gamma. low affinity receptor. involved in a variety of effector and regulatory functions such as phagocytosis of antigen-antibody complexes from the circulation and modulation of antibody production by b-cells. isoforms iib1 and iib1' form caps but fail to mediate endocytosis or	1 92.3 cM	Receptor	
X15592	1.00	1.41	1.00	0.36	1.39	0.16	2.95	0.38	2.62	0.33	cytotoxic T lymphocyte-associated protein 2 beta; Ctla2b	X15592	ctla-2 beta protein precursor (fragment).	not known, expressed in activated t-cell.	13 42.0 cM		
AA500688	1.00	-1.07	1.04	0.63	1.99	0.48	2.68	0.47	2.62	0.21	EST; Unknown	AA500688				EST; Unknown	

Accession	Gene	Protein	CD	Structure	Function	Expression	Receptor
M14215	FCGR3	low affinity immunoglobulin gamma Fc region receptor 3	CD32	type I, monomeric	receptor for the Fc region of complexed immunoglobulins gamma. low affinity receptor.	192.3 cM	
AA212971	FCGR2B	low affinity immunoglobulin gamma Fc region receptor 2B	CD32b	type I, monomeric	binds to the lipid moiety of bacterial lipopolysaccharides (LPS), a glycolipid present in the outer membrane of all gram-negative bacteria. the LPS complex seems to interact with the CD14 receptor.	283.0 cM	
J04694	FCGRI	high affinity immunoglobulin gamma Fc receptor 1	CD64	type I, monomeric	collagen alpha 1 (iv) chain precursor.	85.0 cM	ECM (Matrix Prot)
U55060	FCGRII	high affinity immunoglobulin gamma Fc receptor 2	CD32a	type I, monomeric	galectin-9.		
J05020	FCGRIII	high affinity immunoglobulin gamma Fc receptor 3	CD32c	type I, monomeric	high affinity immunoglobulin epsilon receptor gamma-subunit precursor (FcγRIII)	193.3 cM	Cell Surface Protein
AA023914	FCGRIII	high affinity immunoglobulin gamma Fc receptor 3	CD32c	type I, monomeric	high affinity immunoglobulin epsilon receptor gamma-subunit precursor (FcγRIII)		

U06119	1.00	-1.00	0.51	0.62	1.60	0.49	2.18	0.08	2.56	0.29	cathepsin H; Clsh	U06119	cathepsin h precursor (ec 3.4.22.16) (cathepsin b3) (cathepsin ba).	activation of macrophages by gamma-interferon induces expression of major histocompatibility complex (mhc) class ii genes. an increase in cathepsin h, encoded in the mouse by cish, is also induced by gamma-interferon and	9 50.0 cM	Proteolytic	
D38162	1.00	-2.75	-1.55	0.62	-0.14	1.74	0.58	1.10	2.54	0.31	procollagen, type XI, alpha 1; Coll1a1	D38162	collagen alpha 1(xii) chain precursor.	may play an important role in fibrillogenesis by controlling lateral growth of collagen ii fibrils.	3 53.1 cM	ECM (Matrix Prot)	
AA108054	1.00	-1.40	-0.41	0.50	1.29	0.21	1.78	0.28	2.53	0.24	serine protease inhibitor 6; Spi6	AA108054			13 16.0 cM		
U56819	1.00	-1.28	0.64	0.60	0.83	1.98	4.27	0.29	2.53	0.17	chemokine (C-C) receptor 2; Cmr2	U56819	c-c chemokine receptor type 2 (c-c cr-2) (cc-ckr-2) (ccr-2) (ccr2) (ie/ie receptor) (mcp-1 receptor).	receptor for the mcp-1 (ie), mcp-3 (fic) and mcp-5 chemokines. transduces a signal by increasing the intracellular calcium ions level	9 72.0 cM		
Msa.16995.0	1.00	-1.11	-2.58	2.64	-0.12	1.95	3.20	0.17	2.52	0.46	arachidonate 5-lipoxygenase activating protein	W83564		seems to be required for the activation of 5-lo (5-lipoxygenase). flap could play an essential role in the transfer of arachidonic acid to 5-lo. flap binds to mk-886, a compound that blocks the biosynthesis of leukotrienes		Intracellular Protein	
Msa.88.0	1.00	-2.30	-4.15	2.92	0.09	2.23	1.91	0.28	2.52	0.21	osteoblast specific factor 2; OSF-2	D13664		preferentially expressed in periosteum and periodontal ligament. involved in cell adhesion, highly homologous to beta-ig-h3, a molecule induced by transforming growth factor beta (tgf-beta) that promotes the		Extracellular Protein	

ET62844	1.00	-1.11	0.55	0.84	1.46	0.45	2.77	0.34	2.52	0.33	paired-Ig-like receptor A10,paired-Ig-like receptor A6; Pira10, Pira6	ET62844			7	Receptor	
M33203	1.00	1.33	-0.49	1.58	1.69	2.85	3.74	1.06	2.50	0.63	heme oxygenase (decycling) 1; Hmox1	M33203	heme oxygenase 1 (ec 1.14.99.3) (hox-1) (p32 protein).	heme oxygenase catalyzes the degradation of heme into biliverdin, carbon monoxide, and iron. two forms of this enzyme, heme oxygenase-1 and -2, have been identified; only heme oxygenase-1 is subject to induction by heme, iron, and other factors.	8 C1	Intracellular Protein	
D17630	1.00	-1.27	0.33	0.56	0.10	1.13	2.98	0.37	2.49	1.24	chemokine (C-X-C) receptor 2; Cxcr2	D17630	high affinity interleukin-8 receptor b (il-8r b) (cxcr-2) (gro/mgsa receptor).	receptor to interleukin-8, which is a powerful neutrophils chemotactic factor. binding of il-8 to the receptor causes activation of neutrophils. this response is mediated via a g-protein that activate a phosphatidylinositol-calcium second messenger system. this receptor binds to il-8 with a high affinity and to gro/mgsa and map-2 also with a high affinity.	1 40.0 cM		
U41765	1.00	-1.40	0.41	0.73	0.60	1.70	2.85	0.58	2.48	0.16	a disintegrin and metalloproteinase domain 9 (meltrin gamma); Adam9	U41765			8 8.0 cM		
Msa.1376.0	1.00	1.08	-2.10	1.22	0.19	1.46	1.88	0.21	2.48	0.09	secreted phosphoprotein 1; Spp1	X16151	osteopontin precursor (bone sialoprotein 1) (minopontin) (early t lymphocyte activation 1 protein) (secreted phosphoprotein 1) (spp-1) (2ar) (calcium oxalate crystal growth inhibitor-associated)	binds tightly to hydroxyapatite. appears to form an integral part of the mineralized matrix. probably important to cell-matrix interaction.	5 56.0 cM	Cytokine	

U92437	1.00	-1.85	1.71	0.67	2.06	0.03	2.72	0.35	2.48	0.28	phosphatase and tensin homolog: Pten	U92437	protein-tyrosine phosphatase pten (cc 3.1.3.48) (mutated in multiple advanced cancers)	potential tumor suppressor, active as a phosphatase on tyrosine, serine and threonine residues. no match on blast search 1/99.	19 24.5 cM		
AA667371	1.00	-2.99	-1.56	0.83	-0.40	2.70	0.68	0.93	2.42	0.25	Unknown	AA667371	growth arrest and dna-damage-inducible protein gadd45 gamma (cytokine responsive protein cr6).	plays an important role in negative growth control, including both growth suppression and apoptosis.		EST; Unknown	
Msa.7498.0	1.00	1.38	-0.01	1.13	0.49	1.77	2.90	0.20	2.41	0.37	DNA-damage-inducible, gamma; Gadd45g	AA138777	transcription factor maf2 (proto-oncogene c-maf).	the c-maf interaction site was mapped to the sequence 5'-[gt]gc[n]gt[n]tcag[n]3' in the 17 promoter. it may interact with additional basic-zipper proteins that determine a subtype of maf-responsive element binding	8 61.0 cM	Regulatory	
S74567	1.00	-1.41	3.30	0.41	2.84	1.39	2.88	0.80	2.39	1.21	avian musculoaponeurotic fibrosarcoma (v-maf) AS42 oncogene homolog; Maf	S74567	growth arrest and dna-damage-inducible protein gadd45.	binds to proliferating cell nuclear antigen. might affect pcna interaction with some cdk (cell division protein kinase) complexes; stimulates dna excision repair in vitro and inhibits entry of cells into phase			
AA238081	1.00	-1.19	-1.01	1.19	0.78	2.13	2.04	0.37	2.39	0.24	complement 1, r component; C1r	AA238081	growth arrest and dna-damage-inducible protein gadd45.	marks is the most prominent cellular substrate for protein kinase c. this protein binds calmodulin, actin, and synapsin. marks is a filamentous (f) actin cross-linking protein	6		
W53443	1.00	1.39	-1.66	1.86	0.32	1.35	1.74	0.34	2.38	0.13	GENESEQ:V34267 Human secreted protein gene S8 clone HSSEP68.	W53443	growth arrest and dna-damage-inducible protein gadd45.	also a good match to human clone 2491 (af131781) (both are 89%)		EST; Unknown	
L28177	1.00	1.22	-0.67	1.07	0.03	1.44	5.51	0.19	2.36	0.44	DNA-damage inducible transcript 1; Ddit1	L28177	growth arrest and dna-damage-inducible protein gadd45.	binds to proliferating cell nuclear antigen. might affect pcna interaction with some cdk (cell division protein kinase) complexes; stimulates dna excision repair in vitro and inhibits entry of cells into phase	3 70.5 cM	Intracellular Protein	
Msa.928.0	1.00	-1.07	-1.99	1.35	0.25	1.47	1.88	0.09	2.35	0.18	myristoylated alanine rich protein kinase C substrate; Macs	M60474	myristoylated alanine-rich c-kinase substrate (marks).	marks is the most prominent cellular substrate for protein kinase c. this protein binds calmodulin, actin, and synapsin. marks is a filamentous (f) actin cross-linking protein	10 22.0 cM	Structural Protein	



AA475111	1.00	-1.27	1.20	0.45	1.54	0.12	2.49	0.30	2.31	0.19	heterogeneous nuclear ribonucleoprotein D-EST; Unknown	AA475111							
AA536849	1.00	-1.97	0.31	0.73	3.28	1.85	2.32	0.71	2.31	0.51	EST; Unknown	AA536849						EST; Unknown	
C81524	1.00	-1.20	2.02	0.85	1.09	2.55	1.96	1.84	2.31	1.29		C81524							
AA170245	1.00	1.08	0.79	0.45	0.60	1.69	2.32	0.10	2.30	0.18		AA170245							
AF013262	1.00	-2.69	-0.93	0.72	1.19	2.74	2.01	0.60	2.30	0.72	lumican; Lum	AF013262	lumican precursor (lum) (keratan sulfate proteoglycan).	leucine-rich proteoglycan with keratan sulfate side chains, a major component of cornea, dermal, and muscle connective tissues. regulation of collagen assembly into fibrils in various connective tissues. lumican is necessary in the development of the cornea.	10 61.0 cM	ECM (Matrix Prot)			
AF020313	1.00	-1.73	0.47	0.68	1.07	2.46	3.40	1.07	2.30	0.16	amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein; Apbb1p-binding	AF020313					Extracellular Protein		
Msa.22488.0	1.00	1.08	-1.88	1.54	0.27	2.19	2.75	0.57	2.30	0.22	cathepsin S; Ctsb	AA146437		the cathepsins are mammalian lysosomal cysteine proteinases. they play an important role in protein catabolism within the cell, and may be involved in tumor metastasis.	3 42.7 cM	Proteolytic			
AF004666	1.00	1.09	0.15	0.48	0.11	1.17	2.68	0.32	2.27	0.40	solute carrier family 8 (sodium/calcium exchanger), member 1; Slc8a1	AF004666	sodium/calcium exchanger 1 precursor (na+/ca2+-exchange protein 1).	rapidly transports ca2+ during excitation-contraction coupling. ca(2+) is extruded from the cell during relaxation so as to prevent overloading of intracellular stores.	17 48.0 cM				
Msa.1171.0	1.00	0.63	-0.50	0.61	0.72	2.71	-0.69	1.03	2.27	2.79	keratin-associated protein 5-4; Krtap5-4	M37760							

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Msa.683.0	1.00	-1.85	-0.89	1.02	0.31	1.63	2.14	0.05	2.25	0.17	lectin, galactose binding, soluble 1; Lgals1	W13002	galactin-1 (beta-galactoside-binding lectin 1-14-i) (lactose-binding lectin 1) (s-lac lectin 1) (galaplin) (14 kda lectin).	postimplantation, lgals1 is expressed in somite myotomes, suggesting a role in muscle development. this protein binds beta-galactoside. its physiological function is not yet known. it may act as an autocrine negative growth factor that controls proliferation.	15 44.9 cM	Other
Msa.5619.0	1.00	-1.16	-3.48	2.53	-0.07	2.03	2.48	0.33	2.22	0.22	protease, cysteine, 1; Prsc1	AA000961		a cysteine endopeptidase. legumain was found in all mouse tissues examined, but was particularly abundant in kidney and placenta. the distribution in subcellular fractions of mouse and rat kidney showed a broad localization.		Proteolytic
AA119603	1.00	1.13	1.06	0.58	1.58	0.16	2.17	0.13	2.22	0.30	L1 repeat, Tf subfamily, member 14,L1 repeat, Tf subfamily, member 29; L1Md-Tf14.L1Md-Tf29	AA119603				EST; Unknown
D84391	1.00	-1.58	1.92	0.91	2.05	0.87	1.83	1.73	2.21	1.32						
X16874	1.00	-1.38	-1.89	2.31	0.25	1.88	2.10	0.00	2.17	0.18	complement 1, q subcomponent, beta polypeptide; C1qb	X16874	complement c1q subcomponent, b chain precursor.	the primary humoral mediator of antigen-antibody reactions is the complement (c) system.	4 66.1 cM	Hemostasis
AF022992	1.00	4.47	1.39	0.28	0.21	1.33	1.55	1.17	2.16	0.30	period homolog (Drosophila); Per	AF022992	per-hexamer repeat protein 5,period circadian protein 1 (circadian pacemaker protein mper) (mper)	circadian regulator that may act as a transcription factor. behaves as a negative element in circadian transcriptional loop.	11 B	Other

U69135	1.00	1.15	-7.17	7.77	1.42	0.28	2.76	0.71	2.16	0.11	uncoupling protein 2, mitochondrial; Ucp2	U69135	mitochondrial uncoupling protein 2 (ucp 2) (ucph).	ucp are mitochondrial transporter proteins that create proton leaks across the inner mitochondrial membrane, thus uncoupling oxidative phosphorylation from atp synthesis. as a result, energy is dissipated in the form of heat.	7 50.0 cM	Intracellular Protein	
Msa.4530.0	1.00	1.34	0.13	0.56	1.33	0.21	2.22	0.10	2.16	0.41	EST; region of homology to GENESEQN:Z77537 Human ovarian tumor cDNA library derived	AA106931				EST; Unknown	
Msa.34975.0	1.00	3.11	1.82	0.58	1.92	0.83	2.57	0.42	2.14	0.22	eukaryotic translation initiation factor 2, structural gene Y-linked; Eif2a3y	AA118716	eukaryotic translation initiation factor 2 gamma subunit y-linked (eif-2-gamma y).	eif-2 functions in the early steps of protein synthesis by forming a ternary complex with gtp and initiator trna. this complex binds to a 4s ribosomal subunit, followed by mrna binding to form a 43s preinitiation complex. junction of the 6s ribosomal subunit to form the 8s initiation complex is preceded by hydrolysis of the gtp bound to eif-2 and release of an eif-2-gdp binary complex. in order for eif-2 to recycle and catalyze another round of initiation, the gdp bound to eif-2 must be exchanged with gtp by way of a reaction catalyzed by eif-2b (by	Y	Regulatory	
AA616077	1.00	-1.88	-0.15	0.53	1.56	0.52	2.53	0.27	2.13	0.17		AA616077				EST; Unknown	
AA607513	1.00	-3.27	-3.57	2.01	-0.15	2.43	0.84	0.96	2.13	0.33	Unknown	AA607513				EST; Unknown	
ET62894	1.00	-3.02	0.12	0.95	0.03	1.39	1.03	1.20	2.09	0.16		ET62894				EST; Unknown	

U31993	1.00	1.00	-0.75	0.59	0.42	1.89	2.35	0.25	2.08	0.24	interleukin 17 receptor; IL17r	U31993				6 55.2 cM	Receptor	
Msa.9251.0	1.00	-1.29	-1.33	0.91	0.29	1.90	2.56	0.10	2.05	0.37	neutrophil cytosolic factor 2; Ncf2	AA050149				1 76.1 cM	Intracellular Protein	
Msa.978.0	1.00	-1.00	-1.30	1.35	0.07	1.36	2.07	0.05	2.04	0.24	moesin; Msn	M86390	moesin (membrane-organizing extension spike protein).	thought to work as cross-linkers between plasma membranes and actin-based cytoskeletons. these molecules are involved not only in cytoskeletal organization but also in signal transduction.	X	Cell Surface Protein		
AA474881	1.00	-1.06	1.37	0.61	1.85	0.05	2.66	0.28	2.01	0.20	DNA segment, Chr 1, Wayne State University 40, expressed;	AA474881			1 17.0 cM			
AA204590	1.00	-1.39	0.50	0.54	0.11	1.23	3.51	0.74	2.01	0.31	EST; Unknown	AA204590					EST; Unknown	
AA691533	1.00	-7.45	-1.37	0.88	0.56	2.15	0.50	0.96	2.00	0.50		AA691533					EST; Unknown	
Msa.17862.0	1.00	-6.92	-1.98	0.96	-0.02	1.49	1.85	0.27	1.99	0.12	lysyl oxidase-like; Loxl	W98413				9 33.0 cM		
Msa.29217.0	1.00	-3.11	-1.61	3.81	1.65	0.59	2.80	0.79	1.96	0.30	actin, beta, cytoplasmic	AA079937					Structural Protein	
Msa.24381.0	1.00	-2.44	0.70	0.66	0.52	1.55	2.40	0.55	1.92	0.35	damage specific DNA binding protein 1 (127 kDa); Ddb1	W42399		a dna binding protein that binds specifically to damaged dna. a defect in binding activity is associated with xeroderma pigmentosum e (xpe) in humans.	19 5.0 cM	Other		
X57337	1.00	-2.45	-1.87	0.89	-0.11	1.76	1.39	0.13	1.91	0.19	procollagen C-proteinase enhancer protein; Pcolce	X57337	procollagen c-proteinase enhancer protein precursor (pcpe) (type i)	a glycoprotein that potentiates enzymatic cleavage of the type i procollagen c-propeptide by bone morphogenetic protein-1 (bmp-1)	5 78.0 cM	Extracellular Protein		
Msa.2924.0	1.00	-1.06	-0.71	0.56	0.35	1.36	2.66	0.30	1.91	0.27	superoxide dismutase 3, extracellular; Sod3	X84940	superoxide dismutase [cu-zn]	destroys radicals which are normally produced within the cells and are toxic to biological systems.	5 31.0 cM			
AA608277	1.00	1.72	0.73	0.50	1.21	0.03	2.36	0.18	1.91	0.42		AA608277	1.15.1.1 (ec-sod).					

U75530	1.00	-1.41	3.24	1.00	0.89	2.65	1.99	3.07	1.90	1.73	eukaryotic translation initiation factor 4E binding protein 2; Eif4ebp2	U75530					
M91380	1.00	-2.56	-2.42	1.30	-0.27	1.66	1.64	0.21	1.89	0.10	folistatin-like; Fstl	M91380	folistatin-related protein precursor (tgf-beta-inducible protein tsc-36).	tgfb responsive gene cloned from an osteoblastic cell line. encodes a protein of 35 kda. the amino acid sequence of tsc-36 protein was found to be similar to follistatin, an activin-binding protein, also similar to the secreted	16 27.3 cM	Extracellular Protein	
Msa.21961.0	1.00	-2.48	-0.32	0.79	-0.12	1.13	1.58	0.25	1.89	0.26	EST; Unknown	AA030421		est		EST; Unknown	
Z31334	1.00	-2.57	-3.02	1.52	-0.47	1.96	0.49	0.81	1.84	0.12	procollagen, type I, alpha 2; Cola2	Z31334	collagen alpha 2(i) chain precursor.	type I collagen, the commonest form, is a fibrillar collagen, along with types ii, iii, v, and xl	6 0.68 cM	ECM (Matrix Prot)	
AA176016	1.00	-2.13	0.89	0.73	1.69	0.05	2.43	0.32	1.82	0.19		AA176016					
AA510381	1.00	1.29	1.66	0.99	0.08	1.75	1.14	1.51	1.82	1.19		AA510381					
AA146539	1.00	-1.05	1.80	0.52	1.91	0.05	2.13	0.31	1.78	0.07	EGF-like repeats and discordin I-like domains 3; Edil3	AA146539					
Msa.2536.0	1.00	2.69	-0.19	0.81	1.43	0.08	1.88	0.57	1.74	0.20	extracellular proteinase inhibitor, Expi	X93037	wdm1 protein precursor.	could have proteinase inhibiting capacity.			
D78188	1.00	-2.03	0.04	0.66	0.34	2.02	1.82	0.41	1.74	0.26	granule cell differentiation protein; Gcdp	D78188	myotrophin (v-1 protein) (granule cell differentiation protein).	potential role in cerebellar morphogenesis. may function in differentiation of cerebellar neurons, particularly of granule cells.			
X93037	1.00	3.54	-0.36	0.70	1.60	0.26	1.81	0.49	1.73	0.20	extracellular proteinase inhibitor; Expi	X93037	wdm1 protein precursor.	could have proteinase inhibiting capacity.			

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D50460	1.00	-3.16	-1.78	0.97	0.21	1.47	0.41	0.87	1.67	0.15	stromal cell derived factor 3; Sdf3	D50460	pigment epithelium-derived factor precursor (pdf) (stromal cell-derived factor 3) (sdf-3).	a.k.a pigment epithelium-derived factor -- a member of the serine protease inhibitor (serpin) superfamily, promotes survival and/or differentiation of rat cerebellar granule neurons and human retinoblastoma cells in vitro. no inhibitory activity.	Cytokine	
C76162	1.00	-2.16	0.93	0.55	1.90	0.72	1.59	0.29	1.66	0.22	DNA segment, Chr 10, Johns Hopkins University 81 expressed; D10Jhu81e	C76162				
Msa.27482.0	1.00	-2.98	-0.34	0.93	-0.02	1.68	0.79	0.95	1.63	0.09		AA139094			10 41.7 cM	
X65582	1.00	-2.34	-2.58	0.91	-0.22	1.62	0.31	0.86	1.63	0.20	procollagen, type VI, alpha 2; Col6a2	X65582	collagen alpha 2(vi) chain precursor.	collagen vi acts as a cell-binding protein.	ECM (Matrix Prot)	
X58251	1.00	-2.11	-0.18	0.74	0.01	1.14	0.61	0.89	1.62	0.20	procollagen, type I, alpha 2; Col1a2	X58251	collagen alpha 2(i) chain precursor.	forms the fibrils of tendon, ligaments and bones. in bones the fibrils are mineralized with calcium hydroxvanatite.	ECM (Matrix Prot)	
Msa.22727.0	1.00	-2.67	-0.62	2.27	0.42	1.67	1.45	1.31	1.61	0.93	melanoma X-actin; Actx	AA038134			Structural Protein	
X66405	1.00	-2.18	-3.12	1.32	-0.39	1.72	-0.54	0.85	1.53	0.22	procollagen, type VI, alpha 1; Col6a1	X66405	collagen alpha 1(vi) chain precursor.	collagen vi acts as a cell-binding protein.	ECM (Matrix Prot)	
AF022256	1.00	-3.92	-1.46	0.47	-0.36	1.65	-1.65	1.42	1.49	0.18	keratocan; Kera	AF022256		keratan sulfate proteoglycans (kspgs) play a pivotal role in the development and maintenance of corneal transparency. keratocan, lumican, and mimecan (osteoeclycin) are the major keratins in	ECM (Matrix Prot)	
Msa.22485.0	1.00	-2.42	-0.72	0.53	1.18	0.18	1.79	0.13	1.49	0.07		AA035834				

Msa.2851.0	1.00	-2.52	-4.32	2.71	-0.35	1.82	1.71	0.13	1.46	0.14	lipopolysaccharide binding protein; Lbp	X99347	lipopolysaccharide-binding protein precursor (lbp).	binds to the lipid moiety of bacterial lipopolysaccharides (lps), a glycolipid present in the outer membrane of all gram-negative bacteria. the lbp/lps complex seems to interact with the cell receptor.	2 83.0 cM		
Msa.117.0	1.00	-2.41	-1.85	0.94	-0.06	1.16	1.28	0.10	1.42	0.08	procollagen, type I, alpha 1; Col1a1	U08020	collagen alpha 1(i) chain precursor.	type i collagen is a member of group i collagen (fibrillar forming collagen).	11 56.0 cM	ECM (Matrix Prot)	
Msa.3557.0	1.00	-2.19	-2.73	1.67	-0.28	1.56	-0.45	0.87	1.40	0.19	stromal cell derived factor 3; Sdf3	W08269	pigment epithelium-derived factor precursor (pedf) (stromal cell-derived factor 3) (sdf-3).	neurotrophic protein; induces extensive neuronal differentiation in retinoblastoma cells. as it does not undergo the s (stressed) to r (relaxed) conformational transition characteristic of active serpins, it exhibits no serine protease inhibition.		Cytokine	
L29454	1.00	-2.97	-2.34	0.83	-0.28	1.51	0.42	0.76	1.40	0.16	fibrillin 1; Fbn1	L29454	fibrillin 1 precursor.	structural component of connective tissue microfibrils that binds calcium. fibrillin-1-containing microfibrils provide long-term force bearing structural support.	2 71.0 cM		
AA689977	1.00	-2.14	-0.71	1.22	0.22	1.67	1.16	1.17	1.38	0.10	mini chromosome maintenance deficient 6 (S. cerevisiae); Mcm6	AA689977	dna replication licensing factor mcm6 (mis5 homolog).	may be involved in the control of a single round of dna replication during s phase. binds to chromatin during g1 and detach from it during s phase as if it licenses the chromatin to replicate.			



49

Msa.17592.0	1.00	-2.77	-0.35	0.83	-0.30	1.33	1.52	0.24	0.86	0.65			W96831						
Msa.29918.0	1.00	-2.55	0.41	1.16	-0.02	1.09	1.29	1.17	0.85	0.64	melanoma X-actin; Actx	AA087943							
AA396357	1.00	2.43	-2.33	2.31	0.23	1.34	0.26	0.80	0.71	0.59	ubiquitin-conjugating enzyme E2H; Ube2h complement component 3a receptor 1; C3arl	AA396357					6.65 cM		
U77460	1.00	1.01	-1.80	0.64	-0.72	2.22	3.58	0.80	0.70	0.59		U77460	c3a anaphylatoxin chemotactic receptor (c3a-r) component 3a receptor 1	aka: anaphylatoxin c3a receptor, a g-protein coupled receptor	6 F1			Hemostasis	
Msa.4113.0	1.00	3.13	-1.07	2.02	0.00	2.06	-0.43	1.72	0.69	0.79	glucocorticoid-induced leucine zipper; Gilz	AA050733		expressed in normal lymphocytes from thymus, spleen, and lymph nodes, low or no expression detected in other nonlymphoid tissues, including brain, kidney, and liver. selectively protects t cells from apoptosis induced by treatment with anti-cd				Signal Transduction	
AA222661	1.00	-2.11	-0.06	0.66	-0.09	1.30	-0.44	1.04	0.64	0.61		AA222661							
AA530782	1.00	1.12	-4.81	4.02	-0.29	1.45	-1.23	1.08	0.58	1.24	keratin complex-1, gene C29; Krt1-c29	AA530782				11.57.85 cM			
AF033031	1.00	-0.44	0.93	0.44	0.13	1.15	1.66	1.07	0.56	0.69	solute carrier family 27 (fatty acid transporter), member 2; Slc27a2	AF033031	very-long-chain acyl coa synthetase (ec 6.2.1.-) (very-long-chain- fatty-acid-coa ligase).						
X03986	1.00	1.33	-5.21	1.97	-3.07	1.60	0.63	0.84	0.55	0.56	acetylcholine receptor alpha; Achr	X03986	acetylcholine receptor protein, alpha chain precursor.	the alpha, beta, gamma, and delta subunits of the muscle nicotinic acetylcholine receptor, each encoded by its own locus, are assembled into a pentamer of 2 alpha units and one each of the beta, gamma, and delta	2.43.0 cM		Receptor		
AA611341	1.00	1.31	-2.30	1.59	-0.58	5.09	-3.37	0.47	0.54	1.43	keratin complex-1, gene C29; Krt1-c29	AA611341				11.57.85 cM			
AA240803	1.00	4.90	0.13	0.59	-0.01	2.00	3.35	4.03	0.48	1.55	Unknown, No hits	AA240803						EST; Unknown	
AB007848	1.00	-2.59	-1.24	0.53	0.22	1.88	-0.61	1.14	0.39	0.87	osteomodulin; Omd	AB007848		a novel bone matrix protein.				ECM (Matrix Prot)	

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AA426892	1.00	-2.91	-2.01	0.99	0.18	2.47	-0.02	1.21	0.28	1.23	plasminogen activator, tissue; Plat	AA426892	tissue-type plasminogen activator precursor (ec 3.4.21.68) (tpa) (t-pa) (t-plasminogen activator).	converts the abundant, but inactive, zymogen plasminogen to plasmin by hydrolyzing a single arg-val bond in plasminogen. by controlling plasmin-mediated proteolysis, it plays an important role in tissue remodeling and degradation, in cell migration and many other physiological	89.0 cM		
U16175	1.00	-2.81	-2.68	1.32	-1.31	0.31	-0.68	0.98	0.11	0.73	hypothetical protein, mucin 1, transmembrane, thrombospondin 3; LOC54129, Muc1, Thbs3	U16175	mucin 1 precursor (polymorphic epithelial mucin) (pemit) (episialin), thrombospondin 3 precursor	a secreted glycoprotein member of the class of adhesive proteins. protein appears to have specialized functions in cell growth. thbs3 gene differs markedly from thbs1 and thbs2, both in structure and	3.3 42.6 cM, 3 44.8 cM	Extracellular Protein	
X14194	1.00	-1.05	-2.25	0.71	-0.99	2.19	-0.73	0.96	0.03	0.77	nidogen 1; Nid1	X14194		atp citrate-lyase is the primary enzyme responsible for the synthesis of cytosolic acetyl-coa in many tissues. strongly expressed in liver and adrenal, moderate levels were found in lung, brain, and large intestine. of importance in	13 7.0 cM	Metabolic	
Msa.18310.0	1.00	-2.23	0.10	1.07	0.05	1.53	-0.59	0.93	-0.05	0.74	ATP citrate-lyase	AA000410					

Msa.18226.0	1.00	-2.24	-1.41	1.06	-1.22	0.16	-0.69	0.92	-0.06	0.63	CD34 antigen	AA000252		possible adhesion molecule with a role in early hematopoiesis by mediating the attachment of stem cells to the bone marrow extracellular matrix or directly to stromal cells. could act as a scaffold for the attachment of hematopoietic cells.		Cell Surface Protein	
W40995	1.00	1.18	-3.29	1.32	-1.94	0.73	-0.62	0.85	-0.07	0.70		W40995				EST; Unknown	
U19118	1.00	2.01	-0.96	0.81	-0.83	1.97	-1.82	0.18	-0.09	0.66	activating transcription factor 3; ATF3	U19118	cyclic-amp-dependent transcription factor atf-3 (activating transcription factor 3) (transcription factor lrg-21).	this protein binds the camp response element (cre) (consensus: 5'ggacgt(ac)(a/g)-3'), a sequence present in many viral and cellular promoters. represses transcription from promoters with atf sites. it may repress transcription by stabilizing the binding of inhibitory co-			
Msa.6450.0	1.00	-2.94	-2.22	1.18	-1.31	0.28	-1.43	0.25	-0.13	0.72	early quiescence protein-1; Eql	AA038318					
AA028265	1.00	-2.59	-1.71	1.05	0.65	2.25	-0.62	1.07	-0.13	1.09	fibromodulin	AA028265		fibromodulin, small collagen-binding proteoglycan of the extra-cellular matrix, mainly expressed in articular cartilage, tendon, ligament, leucine-rich repeat (lrr) family believed to function in the assembly of the collagen network in		ECM (Matrix Prot)	

53

X59060	1.00	1.85	-0.94	0.71	-0.32	1.40	4.80	1.20	-0.72	0.81	myogenic factor 6; Myf6	X59060	myogenic factor myf-6 (herculin).	myf6 or herculin is expressed in adult skeletal muscle, but not in smooth muscle, cardiac muscle, or non-muscular tissues. it activates expression of myod1 and myog. the level of expression of herculin is higher than for any of the other	10 59.0 cM	Transcription Factor	
Msa.15200.	1.00	-3.48	-3.48	2.00	-1.38	0.16	-1.75	0.30	-0.72	0.58	CD34 antigen	W65699		possible adhesion molecule with a role in early hematopoiesis by mediating the attachment of stem cells to the bone marrow extracellular matrix or directly to stromal cells. could act as a scaffold for the attachment of		Cell Surface Protein	
AA530179	1.00	1.05	-3.59	2.01	-0.08	2.05	-3.74	0.67	-0.74	1.69	S100 calcium binding protein A3; S100a3	AA530179	s100 calcium-binding protein a3 (s-100e protein).	binds both calcium and zinc. probably binds 2 zinc ions per molecule (by	3 43.6 cM		
Msa.7352.0	1.00	1.81	-2.64	0.53	-0.82	2.09	-0.65	0.85	-0.76	0.70	procollagen, type I, alpha 1	AA008667		type i collagen is of particular importance in the extracellular matrix of bone, skin, tendon, and dentine, and is highly expressed in fibroblasts. it is known to be expressed in mouse palatal shelves		ECM (Matrix Prot)	
AA562685	1.00	-1.16	-2.39	0.61	-0.55	2.04	-0.95	1.17	-0.79	0.84		AA562685		expressed in fibroblasts. it is known to be expressed in mouse palatal shelves			
Msa.723.0	1.00	-2.06	-2.76	1.29	-1.31	0.12	-0.57	0.81	-0.82	0.62	aquaporin 1; Aqp1	L02914	aquaporin-chip (water channel protein for red blood cells and kidney proximal tubule) (aquaporin 1) (early response protein, dar2)	forms a water-specific channel that provides the plasma membranes of red cells and kidney proximal tubules with high permeability to water	6 27.0 cM	Cell Surface Protein	
Msa.17890.	1.00	1.98	-3.38	2.16	-0.23	1.33	-1.21	0.05	-0.86	0.69	eukaryotic translation elongation factor 2; Eef2	W98531					

K02108	1.00	2.14	-0.92	1.29	0.82	1.99	0.19	1.31	-0.86	0.84	keratin complex 2, gene 6a; Krt2-6a	K02108	keratin, type ii cytoskeletal 6 (cyokeratin 6) (k6 keratin).	there are two types of microfilament keratin: i (acidic; 4-55 kda) [k9 to k2] and ii (neutral to basic; 56-7 kda) [k1 to k8]. both a basic and an acidic keratin are required for filament assembly.	15		
AA185284	1.00	2.23	-2.22	0.43	-0.83	1.88	-1.32	0.14	-0.86	0.64		AA185284					
W41417	1.00	3.44	-2.19	1.11	-0.36	1.43	-1.53	0.23	-0.94	0.83		W41417					
Msa.1170.0	1.00	1.37	-3.82	2.50	0.06	2.16	-2.69	0.44	-0.98	1.39	keratin-associated protein 5-1; Krtap5-1	M37759	keratin-associated protein 5-1			Other	
W81858	1.00	1.23	-2.53	0.85	-0.68	1.89	-1.81	1.47	-1.07	0.94	kinesin light chain 1; Klc1	W81858			12.57.0 cM		
C77823	1.00	1.13	-1.83	0.58	-0.57	2.16	-0.67	1.04	-1.08	0.83		C77823					
AF020194	1.00	1.05	-3.83	2.27	-0.41	1.77	-1.05	1.19	-1.08	0.80	taurine/beta-alanine transporter; Taut	AF020194	sodium- and chloride-dependent taurine and beta-alanine transporter.	an amino acid transporter, found primarily in brain.	6.38.2 cM	Cell Surface Protein	
Msa.43191.0	1.00	1.18	-3.36	0.99	-1.28	2.65	-0.86	1.24	-1.09	0.96	integrin-associated protein; Itgp	Z25524					
X63023	1.00	2.54	0.34	0.51	0.25	1.30	-1.13	0.04	-1.14	0.03	cytochrome p450, steroid inducible 3a13; Cyp3a13	X63023	cytochrome p450 3a13 (ec 1.14.14.1) (cyp3a13).	can activate aflatoxin b1 to a genotoxic product.	5		
Msa.22263.0	1.00	-2.02	-1.25	1.32	-0.12	1.28	-0.50	0.92	-1.17	0.11		AA033333					
C80656	1.00	1.58	-3.32	1.44	-0.59	1.91	-0.79	2.01	-1.20	0.87	Unknown	C80656				EST; Unknown	
Msa.1531.0	1.00	1.97	-2.54	1.23	-1.29	0.24	-0.65	0.88	-1.21	0.07	apolipoprotein D; Apod	L39123	apolipoprotein d precursor.	apod occurs in the macromolecular complex with lecithin-cholesterol acyltransferase. it is probably involved in the transport and binding of bilin. appears to be able to transport a variety of ligands in a number of different contexts.	16.21.2 cM	Extracellular Protein	
Msa.9372.0	1.00	1.75	-2.72	1.03	-1.67	0.58	-2.02	0.43	-1.22	0.76	CD59 antigen; Cd59	W41339			2.55.0 cM		

Msa.383.0	1.00	2.36	-1.59	2.09	-0.22	1.48	-1.20	0.07	-1.28	0.12	erythrocyte protein band 4.1; Epb4.1	L00919	protein 4.1 (band 4.1) (p4.1).	protein 4.1 is a major structural element of the erythrocyte membrane skeleton. it plays a key role in regulating membrane physical properties of mechanical stability and deformability by stabilizing spectrin-actin interaction. binds with a high affinity to glycophorin and with lower affinity to band 4.1.	4 65.7 cM	Intracellular Protein	
X82648	1.00	2.15	-1.74	0.84	-1.17	0.14	-0.69	0.88	-1.32	0.08	apolipoprotein D; Apod	X82648	apolipoprotein d precursor.	apod occurs in the macromolecular complex with lecithin-transport and binding of bilin. appears to be able to transport a variety of ligands in a number of different contexts	16 21.2 cM	Other	
Msa.5789.0	1.00	1.98	-3.40	2.07	-0.23	1.46	-0.65	1.07	-1.34	0.16		W18503					
AA673431	1.00	-2.43	-0.84	0.75	0.23	1.52	0.71	1.09	-1.35	0.19		AA673431				EST; Unknown	
Msa.5254.0	1.00	-2.55	-2.67	1.27	-1.48	0.08	-1.88	0.35	-1.43	0.13		AA064307					
Msa.21971.0	1.00	1.10	-4.46	1.91	-1.55	2.64	-0.54	1.03	-1.44	0.12		AA154451					
Msa.14179.0	1.00	2.98	-2.90	1.25	-0.15	1.67	-0.92	1.23	-1.47	0.96	solute carrier family 25 (mitochondrial carrier; peroxisomal membrane protein, 34 kDa), member 17; Slc25a17	AA118682					
AA162560	1.00	1.07	-2.54	0.34	-2.59	0.16	-1.60	0.16	-1.47	0.15		AA162560					
X57024	1.00	1.10	-4.45	2.19	-1.76	0.36	-1.55	0.25	-1.48	0.18	glutamate dehydrogenase; Glud	X57024	glutamate dehydrogenase precursor (ec 1.4.1.3) (gdh).		14 15.5 cM	Metabolic	
AA198316	1.00	2.64	-0.11	0.83	1.38	0.08	0.33	1.10	-1.51	0.18	acyl-CoA thioesterase 1, cytosolic; Cte1-pending	AA198316			12		



Msa.2414.0	1.00	1.72	-2.35	1.26	-0.70	0.64	-1.30	0.17	-1.53	0.19	laminin, alpha 3; Lama3	X84014	laminin alpha-3 chain precursor (fragment).	laminin-5 is thought to be involved in (1) cell adhesion via integrin alpha-3/beta-1 in focal adhesion and integrin alpha-6/beta-4 in hemidesmosomes, (2) signal transduction via tyrosine phosphorylation of pp125-fak and p8, (3) differentiation of keratinocytes (by	18.3.0 cM		
AA237919	1.00	-0.03	-2.41	0.90	-0.29	1.68	-1.58	0.35	-1.53	0.46		AA237919					
AA028657	1.00	1.12	-2.28	0.70	-0.54	1.87	-2.01	0.46	-1.60	1.03	EST; Unknown	AA028657				EST; Unknown	
Msa.330.0	1.00	1.53	-5.88	2.92	-2.03	0.91	-1.61	0.39	-1.63	0.36	upstream transcription factor 2; Usf2	U12283	upstream stimulatory factor 2 (upstream transcription factor 2) (major late transcription factor 2).	bhlh protein that is ubiquitously expressed. that binds to e-boxes (5'-caccg-3') found in a variety of viral and cellular promoters. forms bhlh dimers for dna binding. binds dna as homodimer or heterodimer (usf1/usf2).	7.11.0 cM	Transcription Factor	
Msa.40899.0	1.00	1.40	-2.51	0.86	-1.22	0.17	-3.58	0.96	-1.64	1.30	EST to MYH8	AA162395		m36769 homo sapiens permatat myosin heavy chain 8% to human			
Msa.42549.0	1.00	-2.37	-0.31	1.04	-0.14	1.77	-1.06	1.30	-1.65	0.27	est	AA168690		similar to calmodulin		EST; Unknown	
AA266377	1.00	2.21	-1.86	0.25	-1.53	0.40	-1.67	0.31	-1.69	0.22		AA266377					
Msa.8112.0	1.00	-2.17	-2.20	0.84	-0.38	1.57	-0.54	0.89	-1.71	0.97	CD151 antigen; Cd151	AA050218	platelet-endothelial tetraspan antigen 3 (peta-3) (gp27) (membrane glycoprotein sfa-1) (cd151 antigen).		7.23.5 cM		
D17577	1.00	-2.15	-0.33	0.69	1.25	0.06	-1.82	0.43	-1.72	0.24	kinesin heavy chain member 1B; Kif1b	D17577	kinesin-like protein kif1b.	kif1b works as a monomeric motor for anterograde transport of mitochondria.	4.70.9 cM	Structural Protein	

Msa.2160.0	1.00	1.96	-6.25	5.84	-0.10	1.23	-1.32	0.08	-1.72	0.13	apolipoprotein C1; Apoc1	AA049273	apolipoprotein c-1 precursor (apo-c1).	low molecular weight surface component of chylomicrons and of very low density (vldl) and high density (hdl) lipoproteins. functions may include activation of lecithin:cholesterol acyltransferase, and inhibition of apoe kinase.	7.4.0 cM	Other
U37222	1.00	-2.07	-1.65	0.64	-1.51	0.04	-3.13	1.34	-1.73	0.14	adipocyte complement related protein of 30 kDa; Acp30	U37222	30 kda adipocyte complement-related protein precursor (acrp30) (adipocyte specific protein adi300).	may function as a signaling molecule for adipose tissue.		
AA237797	1.00	1.15	-2.54	0.76	-0.57	1.88	-2.14	0.54	-1.75	1.03	EST; Unknown	AA237797	platelet-endothelial tetraspan antigen 3 (peta-3) (gp27) (membrane glycoprotein sfa-1) (cd151 antigen).		EST; Unknown	
Msa.33047.0	1.00	-2.09	-1.89	0.98	0.71	0.91	1.19	0.14	-1.76	1.51	CD151 antigen; Cd151	AA109912		gene expression was observed in many cell types, but was either absent or present at a low level in brain and lymphoid cells and tissues, including thymus and spleen. contains four putative transmembrane domains, a number of	7.23.5 cM	Cell Surface Protein
Msa.370.0	1.00	1.28	-2.88	0.74	-1.69	0.28	-1.62	0.39	-1.79	0.35	peroxisomal membrane protein 3, 35 kDa; Pmp3	L27842	peroxisome assembly factor-1 (haf-1) (peroxin-2).	somehow implicated in the biogenesis of peroxisomes.		
Msa.13629.0	1.00	1.77	-5.94	4.06	-1.56	0.40	-1.67	0.26	-1.80	0.36		AA155371				
Msa.43204.0	1.00	1.11	-1.96	0.42	-1.63	0.42	-2.18	0.61	-1.85	0.83	serine protease inhibitor 1-1; Spil-1	M75721	alpha-1-antitrypsin 1-1 precursor (serine protease inhibitor 1-1) (alpha-1 protease inhibitor 1) (alpha-1-	inhibitor of serine proteases. its primary target is elastase, but it also has a moderate affinity for plasmin and thrombin.	12.51.0 cM	
D30782	1.00	2.46	-0.98	0.66	-1.36	0.17	-2.84	0.63	-1.85	0.18	epiregulin; Ereg	D30782				
W97690	1.00	1.87	-3.28	1.59	-1.46	0.19	-1.78	0.22	-1.97	0.28		W97690				
Msa.40750.0	1.00	1.20	-2.95	0.51	-1.94	0.71	-1.81	0.34	-2.05	0.38	polypyrimidine tract binding protein 2; Ptb2-pending	AA155318				
AF030001E	1.00	-2.22	-2.62	1.21	-0.40	1.83	-2.62	0.67	-2.06	2.03	Cosmid sequence (>200K)	AF030001				EST; Unknown
NETNX																

Z22661	1.00	2.15	-1.65	0.98	-0.43	1.50	-1.72	0.13	-2.11	0.20	apolipoprotein C-I; Apoc1	Z22661	apolipoprotein c-i precursor (apo-ci).	appears to modulate the interaction of apoe vldl and inhibit binding of beta-vldl to the ldl receptor-related protein	7.40 cM			
Msa.5470.0	1.00	1.04	-1.96	0.78	-1.15	0.14	-3.08	0.53	-2.14	0.38	calsequestrin 1; Casq1	W11481	calsequestrin, skeletal muscle isoform precursor.	calsequestrin is a high-capacity, moderate affinity, calcium-binding protein and thus acts as an internal calcium store in muscle. the release of calcium bound to calsequestrin through a calcium release channel triggers muscle contraction. binds 4 to 5 moles of calcium. also binds		Metabolic		
Msa.43184.0	1.00	1.45	-2.47	0.76	-1.34	0.21	-5.16	1.47	-2.20	1.26	myosin, heavy polypeptide 4, skeletal muscle; Myh4	K00988			11.35.0 cM	Structural Protein		
M32486	1.00	-1.01	-1.21	0.76	-1.29	0.08	-2.24	0.65	-2.22	0.05	hypothetical protein 19.5; p19.5	M32486		geneseqn14534 lov gene (cdna 19.5) - new recombinant polypeptide comprising a t-cell protein - used to regulate t-cell development and tumorigenic phenotype and to block t-cell activation in auto-immune disease. patent held by		Patented; Novel		
X90875	1.00	1.47	-3.41	1.29	-2.40	0.52	-2.34	0.43	-2.23	0.14	fragile X mental retardation gene, autosomal homolog; Fxr1h	X90875						
W11010	1.00	2.04	-1.68	0.59	-1.49	0.05	-1.88	0.32	-2.24	0.17	region of homology to: cell division cycle 4-like; beige-like;	W11010					Regulatory	

U30840	1.00	1.36	-1.71	0.55	-1.49	0.32	-1.88	0.17	-2.25	0.09	voltage-dependent anion channel 1; Vdac1	U30840	voltage-dependent anion-selective channel protein 1 (mvdac1) (outer mitochondrial membrane protein porin 1).	forms a channel through the mitochondrial outer membrane that allows diffusion of small hydrophilic molecules. the channel adopts an open conformation at low or zero membrane potential and a closed conformation at potentials above 3-4 mv. the open state has a weak anion selectivity whereas the closed state is cation-	11 29.0 cM		
J03398	1.00	-1.60	-2.11	0.74	-1.32	0.07	-4.66	0.85	-2.29	1.31	P glycoprotein 2; Pgy2	J03398	multidrug resistance protein 2 (p-glycoprotein 2).	mdr gene encoding a multidrug resistance protein mdr	5 1.0 cM	Cell Surface Protein	
X61433	1.00	1.06	-1.90	0.33	-1.48	0.10	-2.09	0.36	-2.30	0.12	ATPase, Na <sup>+</sup> /K <sup>+</sup> transporting, beta 1 polypeptide; Alp1b1	X61433	sodium/potassium-transporting atpase beta-1 chain (sodium/potassium-dependent atpase beta-1 subunit).	expressed in brain, kidney, lung, testis, and heart. not found in the liver. expression occurs in pre-b lymphocytes, resting b cells in the bone marrow, pre-t cells, and mature thymocytes. mitogen-stimulated t and b cells.	1 86.8 cM	Cell Surface Protein	
Msa.2879.0	1.00	1.32	-2.74	1.40	-1.53	0.12	-2.62	0.14	-2.31	0.27	transducer of ErbB-2.1; Tob1	D78382	tob protein (transducer of erb-2).	anti-proliferative protein that interacts with the erb-2 receptor tyrosine kinase. may physically and/or functionally interact with protein-tyrosine kinase receptors (by simulating)			

X06115	1.00	1.44	-1.93	0.73	-1.54	0.07	-1.83	0.07	-2.31	0.24	cadherin 1; Cdh1	X06115	epithelial-cadherin precursor (e-cadherin) (uvomorulin) (arc-1).	cadherins are calcium dependent cell adhesion proteins. they preferentially interact with themselves in a homophilic manner in connecting cells; cadherins may thus contribute to the sorting of heterogeneous cell	8 53.3 cM		
Msa.3250.0	1.00	1.14	-4.21	2.32	-1.75	0.48	-1.66	0.34	-2.32	0.40	histidyl tRNA synthetase; Hars	U39473	histidyl-tRNA synthetase (ec 6.1.1.21) (histidine--tRNA ligase) (hirs).				
Msa.29324.0	1.00	1.63	-1.48	1.37	-1.32	0.26	-2.00	0.18	-2.33	0.11		AA080197					
Msa.4067.0	1.00	1.73	-2.15	0.61	-0.72	1.74	-0.78	1.03	-2.34	0.57	Sip1?	AA003876		splicing factor (homosapiens)		Unknown	
Msa.5481.0	1.00	1.28	-2.81	1.61	-1.56	0.02	-2.00	0.09	-2.35	0.13	annexin A8; Anxa8	AA060106			14 13.0 cM	EST; Unknown	
AB000713	1.00	-0.50	-1.12	1.24	1.23	0.05	-1.86	0.34	-2.35	0.72	claudin 4; Cldn4	AB000713	claudin-4 (clostridium perfringens enterotoxin receptor) (cpe-receptor) (cpe-r).	a 4 transmembrane domain protein that is a novel component of tight junction strands of liver and kidney.	5 75.0 cM	Cell Surface Protein	
AA615066	1.00	2.07	-4.34	2.32	-0.57	1.61	-1.58	0.35	-2.38	0.54		AA615066					
Msa.39064.0	1.00	1.13	-2.50	1.11	-1.58	0.22	-2.58	0.28	-2.39	0.18	titin (series elastic element of striated muscle)	AA145312		titin, giant sarcomeric protein, extending from the m line to the z line of striated muscle sarcomere, essential in the temporal and spatial control of the assembly of the highly ordered sarcomeres of striated muscle.		Structural Protein	



Msa.570.0	1.00	1.28	-3.02	2.47	-0.25	1.42	-2.54	0.82	-2.43	0.44	gap junction membrane channel protein beta 2; Gjb2	M81445	gap junction beta-2 protein (cx26).	one gap junction consists of a cluster of closely packed pairs of transmembrane channels, the connexons, through which materials of low mw diffuse from one cell to a neighboring cell.	14 21.0 cM	
C77662	1.00	1.30	-2.44	0.87	-1.40	0.22	-2.48	0.29	-2.44	0.36	Rev-ErbA-alpha protein; rat	C77662		most similar in structure to the thyroid hormone receptor (c-erbA) and the retinoic acid receptor, but it does not bind either thyroid hormone or retinoic acid. the mrna encoding rev-erbA alpha is present in many tissues and is particularly a	Receptor	
Msa.3940.0	1.00	-1.09	-2.21	0.57	-1.72	0.18	-2.20	0.33	-2.44	0.12		W13191				
AA690434	1.00	1.12	-1.86	0.32	-1.84	0.50	-2.52	0.38	-2.45	0.11		AA690434	microtubule-associated protein 4;	non-neuronal microtubule-associated protein. promotes microtubule	9 58.0 cM	
M72414	1.00	1.68	-4.09	1.85	-2.21	0.09	-2.62	0.48	-2.47	0.24	microtubule-associated protein 4; Mtap4	M72414				
Msa.799.0	1.00	-1.57	-3.69	1.19	-2.69	0.73	-2.24	0.25	-2.48	0.30	interferon-related developmental regulator 1; Ifrd1	J00424	interferon-related developmental growth factor-inducible protein pc4) (tpa induced sequence 7) (tis7 protein).	could play a role in regulating gene activity in the proliferative and/or differentiative pathways induced by ngf. may be an autocrine factor that attenuates or amplifies the initial ligand		Cytokine
W29651	1.00	1.11	-4.23	2.14	-1.98	0.01	-2.48	0.34	-2.48	0.30		W29651				
AA688835	1.00	-1.76	-3.43	1.28	-1.97	0.08	-2.48	0.61	-2.51	0.10	Unknown	AA688835			EST; Unknown	
AJ001118	1.00	1.17	-2.97	0.97	-2.10	0.28	-2.89	0.25	-2.56	0.14	monoglyceride lipase; Mgl1	AJ001118			3	
Msa.19265.0	1.00	2.33	-2.61	0.87	-1.88	0.75	-1.96	0.52	-2.57	0.53	golgi autoantigen, golgn subfamily a, 4; Golga4	AA009086				
AF026489	1.00	1.67	-2.26	0.77	-1.75	0.32	-2.22	0.24	-2.62	0.19	beta-spectrin 3; Spnb3	AF026489			19 0.0 cM	
Msa.28719.0	1.00	1.54	-3.87	1.00	-3.39	1.49	-2.22	0.10	-2.65	0.05		AA072611				

Msa.9757.0	1.00	1.17	-7.61	6.54	-1.66	0.42	-2.17	0.25	-2.67	0.19	basic transcription element binding protein 2; KlF5 desmocollin 1; Dsc1	AA014295	desmocollin 1a/1b precursor.	component of intercellular desmosome junctions. involved in the interaction of plaque proteins and intermediate filaments mediating cell-cell adhesion. may contribute to epidermal cell positioning (stratification) by mediating differential adhesiveness between cells that express different isoforms. linked to the			
X97986	1.00	1.11	-1.97	1.84	-1.42	0.40	-3.01	1.27	-2.71	0.34		X97986					
Msa.32581.0	1.00	1.41	-2.38	1.08	-1.25	0.21	-2.58	0.43	-2.72	0.11	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4; Slc25a4	AA107658	adp.atp carrier protein, heart/skeletal muscle isoform t1 (adp/ATP translocase 1) (adenine nucleotide translocator; complement factor d precursor (ec 3.4.21.46) (c3 convertase activator) (properdin factor d) (adipsin) (28 kDa protein; adipsin)	carries adenosine triphosphate (ATP) from the mitochondrial matrix into the intermembrane space and the diphosphate (ADP) in the reverse a serine protease synthesized principally in adipose tissue, but also by sciatic nerve... adipsin is suppressed (more than 1-fold) in genetically obese mice	8 26.0 cM	Other	
Msa.450.0	1.00	-1.56	-3.38	1.69	-1.73	0.11	-4.22	2.40	-2.74	0.20	adipsin; Adn	W36455			10 43.0 cM	Proteolytic	
Msa.11196.0	1.00	1.31	-1.76	0.72	-1.74	0.44	-1.70	0.37	-2.74	0.24		W50088					
U06670	1.00	1.16	-2.84	1.03	-1.65	0.01	-3.54	1.46	-2.75	0.44	very low density lipoprotein receptor; Vldlr	U06670	very low-density lipoprotein receptor precursor (vldl receptor).	binds vldl and transports it into cells by endocytosis. in order to be internalized, the receptor-ligand complexes must first cluster into clathrin-coated pits	19 20.0 cM	Receptor	

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Msa.23977.0	1.00	1.39	-2.52	1.29	-1.22	0.04	-2.57	0.68	-2.76	0.26	EST	W07946			geneseqn:z9721 human secreted protein gene 3 cdna clone hwhgu54, seq id no:13. new isolated human genes and the secreted treatment of e.g. cancers.			
W71831	1.00	1.37	-5.51	3.22	-1.70	0.18	-3.58	1.40	-2.76	0.36	histone deacetylase 5; Hdac5	W71831						
U12785	1.00	1.04	-2.41	0.64	-1.96	0.28	-2.62	0.39	-2.77	0.07	alcohol dehydrogenase family 3, subfamily A1; Aldh3a1	U12785	aldehyde dehydrogenase, dimeric nadp-preferring (ec 1.2.1.5) (aldh class 3) (dioxin-inducible aldehyde dehydrogenase-3); fatty aldehyde dehydrogenase (ec 1.2.1.3) (aldehyde dehydrogenase, microsomal) (aldh class 3).	aldhs play a major role in the detoxification of alcohol-derived acetaldehyde. they are involved in the metabolism of corticosteroids, biogenic amines, neurotransmitters, and lipid peroxidation. this protein preferentially oxidizes aromatic aldehyde substrates. it may play a role in the oxidation of toxic	11 34.25 cM			
AA462409	1.00	1.14	-1.61	1.30	-1.49	0.25	-2.23	0.31	-2.81	0.04	Unknown	AA462409					EST;	Unknown
Msa.4575.0	1.00	-1.01	-2.05	1.68	-1.47	0.36	-2.53	0.73	-2.81	0.20	EST	AA065868			geneseqn:z56885 human sbpsapl polypeptide encoding est derived sequence. new polypeptides of prosaposin family, antagonist and inhibitors for treatment			
Msa.16748.0	1.00	2.17	-2.91	1.31	-1.55	0.39	-2.81	0.81	-2.83	0.59		W78443						
Msa.3237.0	1.00	1.01	-2.22	1.69	-1.64	0.57	-1.49	0.07	-2.83	0.29	four and a half LIM domains 1; Fhl1	W14830			fhl1 and fhl3 were expressed in a number of skeletal muscles while fhl2 was expressed at high levels in cardiac muscle. may have an involvement in muscle development or	X A6-A7.1	Regulatory	

AA028770	1.00	0.02	-2.96	1.22	-0.34	1.56	-2.74	0.63	-2.86	1.02	Cysteine Rich protein 2, rat	AA028770				Regulatory
M91236	1.00	1.28	-2.27	1.21	-1.61	0.53	-2.93	1.20	-2.86	0.27	gap junction membrane channel protein beta 5; Gjb5	M91236	gap junction beta-5 protein (connexin 30.3) (cx30.3).	one gap junction consists of a cluster of closely packed pairs of transmembrane channels, the connexons, through which materials of low mw diffuse from one cell to a neighboring cell	4 57.5 cM	
W62701	1.00	1.71	-3.09	2.19	-0.68	0.74	-2.36	0.14	-2.88	0.52		W62701				
Msa.6594.0	1.00	1.58	-1.24	1.11	-0.37	1.53	-4.56	2.63	-2.92	0.36		W30612				
Msa.7275.0	1.00	1.19	-1.82	1.28	-1.28	0.03	-2.67	0.32	-2.95	0.31	Mus musculus phosphofructokinase-1 A isozyme (Pfkfb1)	W17917				
Msa.26512.0	1.00	1.31	-1.53	1.17	-1.38	0.29	-2.28	0.39	-3.01	0.48	tubulin alpha 8; Tubaa8	AA063914				
X13135	1.00	1.12	-4.53	1.73	-2.16	0.14	-3.08	0.44	-3.06	0.45	fatty acid synthase; Fasn	X13135	fatty acid synthase (ec 2.3.1.85) [includes: ec 2.3.1.38; ec 2.3.1.39; ec 2.3.1.41; ec 1.1.1.100; ec 4.2.1.61; ec 1.3.1.10-ec	fatty acid synthase (fas) catalyzes the last step in the fatty acid biosynthetic pathway.	11 72.0 cM	Metabolic
Msa.3669.0	1.00	-1.55	-1.69	0.98	-1.64	0.34	-2.26	0.62	-3.06	0.28	est	W08486				EST; Unknown
AA138388	1.00	1.25	-2.10	0.49	-1.90	0.24	-1.97	0.25	-3.07	0.63		AA138388				
U62295	1.00	1.09	-3.22	1.18	-1.83	0.38	-2.99	0.47	-3.07	0.10	cytochrome P450, 2j6; Cyp2j6	U62295	cytochrome p450 2j6 (ec 1.14.14.1) (cyp1j6) (arachidonic acid epooxygenase).		4 46.5 cM	
Msa.2753.0	1.00	-1.18	-5.10	2.45	-1.92	0.61	-2.80	0.31	-3.08	0.53	laminin, beta 2; Lamb2	U43541	laminin beta-2 chain precursor.	extracellular matrix glycoproteins which are major components of basement membranes	9 60.0 cM	ECM (Matrix Prot)
AA734300	1.00	1.09	-2.42	0.84	-1.93	0.62	-2.71	0.59	-3.10	0.48	Hypothetical protein FLJ20171, human	AA734300				Unknown

Msa.717.0	1.00	-1.17	-4.27	2.07	-1.93	0.53	-5.02	1.56	-3.12	0.59	glycerolphosphate dehydrogenase 1, cytoplasmic adult; Gdc1	M13366	glycerol-3-phosphate dehydrogenase [nad+], cytoplasmic (ec 1.1.1.8) (gpd-c) (mdh-c)	belongs to the nad-dependent glycerol-3-phosphate dehydrogenase family.	15 56.8 cM	Metabolic	
AA409316	1.00	1.83	-2.55	1.34	-1.53	0.46	-3.69	0.33	-3.12	0.71		AA409316					
Msa.12516.0	1.00	1.38	-2.89	1.39	-1.30	0.19	-2.89	0.42	-3.12	0.54	Unknown	W55004				Unknown	
Msa.41264.0	1.00	1.77	-5.60	2.99	-1.66	0.56	-7.59	2.64	-3.17	1.80	myosin heavy chain EST to	AA162315		myh8		Structural Protein	
L04678	1.00	1.47	-3.65	1.95	-1.38	0.37	-1.80	0.40	-3.18	0.26	integrin beta 4; Itgb4	L04678			11 76.0 cM		
Z22866	1.00	1.92	-2.24	0.85	-1.62	0.34	-3.33	0.70	-3.19	0.76	myomesin 1; Myom1	Z22866					
Msa.726.0	1.00	1.50	-3.07	1.42	-1.49	0.04	-2.21	0.08	-3.21	0.73	glutathione-S-transferase, alpha 2 (Yc2); Gsta2	W29265	glutathione s-transferase g41a (ec 2.5.1.18) (gst class-alpha)	liver enzyme;	9 44.0 cM	Metabolic	
U31510	1.00	1.18	-4.17	2.06	-2.06	0.23	-1.40	1.32	-3.21	0.39	ADP-ribosyltransferase 1; Art1	U31510	gpi-linked nad(p+)-arginine adp-ribosyltransferase precursor (ec 2.4.2.31) (mono(adp-ribosyl)transferase) (yac-1), poly [adp-ribose] polymerase (ec 2.4.2.30) (parp) (adprt) (nad+) adp-ribosyltransferase (poly[adp-ribose] synthetase).	poly[adp-ribose] polymerase modifies various nuclear proteins by poly(adp-ribose)ylation. the modification is dependent on dna and is involved in the regulation of various important cellular processes such as differentiation, proliferation, and tumor transformation and also in the regulation of the molecular events involved in the recovery of cell from	7 50.0 cM	Metabolic	
Msa.3511.0	1.00	2.20	-1.47	0.57	0.08	1.27	-1.85	0.37	-3.23	0.71	aldolase 3, C isoform; Aldo3	W53351	fructose-bisphosphate aldolase c (ec 4.1.2.13) (brain-type aldolase) (fragment1)		11 44.98 cM		
AA691651	1.00	1.12	-2.64	0.65	-1.94	0.58	-2.90	0.47	-3.24	0.30	EST; Unknown	AA691651				EST; Unknown	
X51905	1.00	1.55	-5.30	3.66	-1.51	0.09	-2.88	0.28	-3.28	0.36	lactate dehydrogenase 2, B chain; Ldh2	X51905	l-lactate dehydrogenase h chain (ec 1.1.1.27) (ldh-b)		6 62.0 cM	Metabolic	
W15862	1.00	1.30	-1.53	0.84	-1.60	0.30	-3.12	0.84	-3.29	0.40	uncoupling protein 2, mitochondrial; Ucp2	W15862	mitochondrial uncoupling protein 2 (ucp 2) (ucph).	blast of 12/99 = no match	7 50.0 cM	Intracellular Protein	

Msa.30092.0	1.00	1.23	-8.99	6.81	-1.44	0.05	-5.46	1.82	-3.29	0.54	myosin, heavy polypeptide 3, skeletal muscle, embryonic; Myh3	AA089202	myosin heavy chain, fast skeletal muscle, embryonic (fragment).	muscle contraction.	11 35.0 cM		
Msa.23986.0	1.00	-1.13	-2.92	0.87	-1.80	0.13	-3.03	0.46	-3.30	0.65	EST to LTRP4	W16389	latent transforming growth factor 6% nucleotide level				
AA423082	1.00	1.23	-2.92	0.98	-1.73	0.72	-2.72	0.71	-3.37	0.72	Unknown	AA423082				EST; Unknown	
Msa.21797.0	1.00	1.31	-2.77	0.75	-1.85	0.02	-3.30	0.31	-3.44	0.32	ADP-ribosyltransferase 3 (Art3)	AA028701				Other	
Msa.1286.0	1.00	1.60	-3.15	1.51	-2.15	0.66	-6.37	2.47	-3.45	1.64	wingless-related MMTV integration site 4; Wnt4	M89797	wnt-4 protein precursor.	may be an intracellular signaling molecule involved in segmentation of the forebrain. is likely to signal over only few cell diameters (by similarity). seems to be involved in kidney development.	14		
X51829	1.00	1.04	-4.58	2.18	-2.40	0.50	-2.90	0.28	-3.48	0.39	myeloid differentiation primary response gene 116; Myd116	X51829	myeloid differentiation primary response protein myd116.			Other	
Msa.3168.0	1.00	1.09	-3.46	1.73	-1.64	0.00	-2.65	0.18	-3.66	0.88	gap junction membrane channel protein beta 6; Gjb6	Z70023	one gap junction consists of a cluster of closely packed pairs of transmembrane channels, the connexons, through which materials of low mw diffuse from one cell to a neighboring cell.		14		
ET62740	1.00	2.18	-2.68	0.86	-2.03	0.73	-2.43	0.60	-3.69	0.95	ankyrin 3, epithelial; Ank3	ET62740			10 38.0 cM		
M74495	1.00	-1.28	-1.86	1.37	-1.22	0.02	-2.60	0.64	-3.70	0.25	adenylosuccinate synthetase 1, muscle; Adss1	M74495	adenylosuccinate synthetase, muscle isozyme (ec 6.3.4.4) (imp-- aspartate ligase) (adss) (amnsase).	plays an important role in the de novo pathway of purine nucleotide biosynthesis.			
AA407234	1.00	1.93	-2.78	0.47	-2.39	1.02	-3.71	1.15	-3.74	0.79		AA407234					

U76618	1.00	1.16	-1.51	1.02	-1.52	0.24	-1.60	0.21	-3.77	0.45	nebulin-related anchoring protein; Nrap	U76618	specific to skeletal and cardiac muscle, not detected by northern blot in non-muscle. localized at myotendinous junction in mouse skeletal muscle and intercalated disc in cardiac muscle. plays a role in anchoring laminin.	19 53.25 cM	Structural Protein	
AA717225	1.00	-1.07	-2.01	0.52	-1.49	0.03	-2.85	0.77	-3.80	0.63		AA717225				
Msa.15880.0	1.00	-5.84	-2.18	1.33	-1.49	0.24	-2.09	0.30	-3.81	0.73	neuropeptide Y; NPY	W70782	implicated in the control of feeding and in secretion of gonadotrophin-release hormone.		Other	
M81086	1.00	1.11	-2.08	0.96	-1.62	0.39	-5.80	3.35	-3.82	0.31	tropomyosin 2, beta; Tpm2	M81086	an actin-associated cytoskeletal protein. different isoforms occur in skeletal muscle and in smooth muscle and nonmuscle cells.		Structural Protein	
AF026072	1.00	-0.16	-1.09	1.73	-0.29	1.69	-2.40	1.47	-3.83	1.01	hydroxysteroid sulfotransferase; SUL12B	AF026072				
C80836	1.00	1.45	-3.34	1.10	-2.41	0.17	-6.22	1.90	-3.83	1.08	EST; unknown	C80836			EST; Unknown	
AA265119	1.00	-2.16	-2.71	0.67	-2.32	0.55	-6.91	3.49	-3.90	0.53	EST; Unknown	AA265119			EST; Unknown	
D42048	1.00	-1.41	-1.83	1.36	-1.80	0.64	-2.87	0.48	-3.92	0.40	squalene epoxidase; Sqle	D42048	squalene monooxygenase (ec 1.14.99.7) (squalene epoxidase) (se).			
													catalyzes the first oxygenation step in sterol biosynthesis and is suggested to be one of the rate-limiting enzymes in this pathway.			
Msa 400.0	1.00	1.24	-4.47	1.71	-2.24	0.01	-4.10	0.65	-3.98	0.71	myosin heavy chain, cardiac muscle, adult; Myhca	M76601	myosin heavy chain, cardiac muscle alpha isoform.	14 20.0 cM	Structural Protein	
U76371	1.00	1.17	-1.64	1.11	-0.08	1.23	-4.77	1.17	-4.01	1.08	CD8beta opposite strand; Bop	U76371	a transcribed gene designated as bop, is a cd8-beta opposite direction transcript. detected in mouse thymus only, and may be limited to cd8+ t cells.	6 30.5 cM	Other	



Msa.6099.0	1.00	1.55	-3.68	1.82	-0.34	1.40	-6.77	1.74	-4.65	1.17	histidine rich calcium binding protein; Hrc	W13030		a striated muscle sarcolemmal reticulum (sr) membrane protein. rapid release and uptake of intracellular calcium is the function of the sr. luminal sr proteins are presumed to function in calcium storage and in coordination of calcium release.	7 20.4 cM	Regulatory	
AA611262	1.00	1.31	-2.81	0.93	-1.84	0.29	-2.72	0.73	-4.75	0.18	N-myc downstream regulated 2; Ndr2	AA611262	ndrg2 protein (ndr2 protein).	(human ndr2).			
Y09257	1.00	-1.07	-3.31	1.28	-2.41	0.78	-8.29	2.99	-4.78	0.84	nephroblastoma overexpressed gene; Nov	Y09257	nov protein homolog precursor (novh).	protein likely to play a role in cell growth regulation (by similarity).	15 22.5 cM	Signal Transduction	
Msa.728.0	1.00	1.48	-3.39	1.24	-1.69	0.49	-6.12	1.21	-4.91	1.03	solute carrier family 2 (facilitated glucose transporter), member 4; Slc2a4	M23383	glucose transporter type 4, insulin-responsive (gt2).	insulin-responsive glucose carrier protein isoform, glut4. specific to adipose tissue and to skeletal muscle and cardiac muscle.	11 40.0 cM	Cell Surface Protein	
ET61471	1.00	1.77	-5.58	1.40	-5.83	2.05	-3.66	0.36	-4.99	0.57	mast cell protease 7; Mcpt7	ET61471	mast cell protease 7 precursor (cc 3 4.21.) (mmcp-7) (trypsin).		17 10.4 cM		
Msa.4287.0	1.00	1.32	-3.52	1.57	-1.82	0.09	-6.75	1.84	-5.01	0.68	apolipoprotein B editing complex 2; Apobec2	W29506		apobec-2 mma and protein are expressed exclusively in heart and skeletal muscle. apobec-2 does not display detectable apob mma editing activity. has low, but definite, intrinsic cardiolipin desaturase activity.	17 24.0 cM	Intracellular Protein	
M76601	1.00	1.25	-6.73	3.31	-2.47	0.03	-4.62	0.66	-5.31	0.60	myosin heavy chain, cardiac muscle, adult; Myhca	M76601	myosin heavy chain, cardiac muscle alpha isoform.	adult cardiac specific isoform of myosin heavy chain. (see additional information for regulation).	14 20.0 cM	Structural Protein	
X99251	1.00	1.56	-1.54	1.06	-1.59	0.49	-4.38	1.31	-5.36	1.03	repetin; Rptm	X99251	repetin.	novel potential precursor protein of the cornified cell envelope.	3		
Msa.8838.0	1.00	-1.35	-2.43	0.83	-2.79	0.11	-2.90	0.50	-5.40	1.19	myosin light chain, alkali, cardiac ventricles; Mylc	W34697			9 61.0 cM	Structural Protein	

Msa.13213.0	1.00	1.37	-5.96	3.66	-1.84	0.19	-5.66	0.99	-5.68	0.86	actinin alpha 2; Actn2	W53582	junction plakoglobin (desmoplakin iii) (fragment).	one of the proteins of desmosomal membrane anchorage site plaques of the epithelium, and is also a component of plaques of the adherens junction	13 7.0 cM	Structural Protein	
Msa.2776.0	1.00	1.32	-3.40	1.87	-1.41	0.24	-2.27	0.48	-6.03	1.83	junction plakoglobin (desmoplakin iii) (fragment).	M90365	junction plakoglobin (desmoplakin iii) (fragment).	one of the proteins of desmosomal membrane anchorage site plaques of the epithelium, and is also a component of plaques of the adherens junction	11 60.0 cM	Structural Protein	
AA562768	1.00	2.21	-7.37	1.45	-3.74	2.31	-7.62	2.96	-6.40	1.95	glioblastoma amplified sequence; Gbas	AA562768				Other	
Msa.2946.0	1.00	1.13	-4.57	1.95	-2.15	0.90	-2.87	0.34	-6.70	0.89	cysteine-rich protein 3; Crp3	W08774	ccat/enhancer binding protein delta (c/ebp delta) (c/ebp-related protein 3), lmn domain protein, cardiac (muscle lmn protein) (cysteine-rich protein 3)	cardiac lmn protein		Transcription Factor	
Msa.727.0	1.00	1.74	-5.46	1.82	-3.53	0.55	-5.48	1.18	-6.92	1.19	glutathione-S-transferase, alpha 3; Gsta3	M73483	glutathione S-transferase yc (ec 2.5.1.18) (gst class-alpha).	conjugation of reduced glutathione to a wide number of exogenous and endogenous hydrophobic electrophiles. this gst has a high catalytic activity for aflatoxin	9 48.0 cM	Metabolic	
Msa.27462.0	1.00	-1.46	-4.50	1.10	-4.40	1.47	-4.02	1.38	-7.09	1.40	growth hormone receptor; Ghr	AA066700	high molecular weight growth hormone receptor/binding protein precursor, low molecular weight growth hormone receptor/binding protein precursor	binding of gh to ghr activates insulin-like growth factor 1 (igf1), which in turn binds to its own receptor to activate signal-transduction pathways leading to growth	15 4 6 cM	Receptor	
Msa.540.0	1.00	1.21	-5.09	2.84	-1.82	0.51	-5.41	1.45	-7.23	1.37	gap junction membrane channel protein beta 4; Gjb4	M91443	gap junction beta-4 protein (connexin 31.1) (cx31.1).	one gap junction consists of a cluster of closely packed pairs of transmembrane channels, the connexons, through which materials of low mw diffuse from one cell to a neighboring cell	4 57.5 cM		



Msa.4623.0	1.00	1.37	-6.95	3.61	-1.82	0.25	-8.69	2.10	-7.51	0.45	actinin alpha 2; Actn2	W34429			13 7.0 cM	Structural Protein	
X91825	1.00	1.35	-3.03	1.34	-2.07	0.56	-5.10	0.64	-7.86	1.18	small proline-rich protein 1B; Spr1b	X91825	comin b (small proline-rich protein 1b) (spr1b) (spr1b)	cross-linked envelope protein of keratinocytes. it is a keratinocyte protein that first appears in the cell cytosol, but ultimately becomes cross-linked to membrane proteins by transglutaminase. all that results in the formation of an insoluble envelope beneath the plasma	3 45.2 cM		
Msa.17804.0	1.00	-5.76	-4.91	2.21	-1.68	0.14	-4.53	1.89	-8.12	1.86	synuclein, gamma; Snca	AA108571			14 12.5 cM		
Msa.9519.0	1.00	1.22	-10.56	7.86	-1.87	0.70	-10.02	4.21	-8.45	0.47	actinin alpha 2; Actn2	W40754		alpha-actinin 2 mrna,	13 7.0 cM	Structural Protein	
Msa.22711.0	1.00	-1.16	-1.54	1.75	1.07	0.03	-9.74	1.39	-8.51	2.35	creatine kinase; mitochondrial 2 (sarcomeric)	AA038095		reversibly catalyzes the transfer of phosphate between ap and various phosphogens (e.g. creatine phosphate). creatine kinase isoenzymes play a central role in energy transduction in tissues with large, fluctuating energy demands, such as muscle		Metabolic	
Msa.20143.0	1.00	1.25	-2.76	2.09	-0.75	1.88	-4.08	0.93	-9.86	1.89	hydroxysteroid sulfotransferase; SULT2B	AA016485					
Msa.4317.0	1.00	2.43	-6.26	3.80	-1.72	0.38	-2.62	0.21	-11.22	4.05	calcium channel, voltage-dependent, gamma subunit 1; Cagng1	AA061886				Cell Surface Protein	
Msa.24682.0	1.00	1.46	-4.33	1.40	-2.98	0.65	-9.23	0.73	-11.22	1.05	ART3 (ADP-ribosyltransferase 3)	W82798		gonococci: testis specific.		Intracellular Protein	
M88694	1.00	15.59	-3.05	2.20	-0.50	1.50	-6.42	4.80	-11.31	4.10	thioether S-methyltransferase, Temt	M88694	thioether S-methyltransferase (ec 2.1.1.96) (temt).	catalyzes transfer of the methyl group from S-adenosylmethionine to x in compounds of the structure r-x-r', where x may be sulfur, selenium, or tellurium, and r and r' may be various organic		Other	

X79199	1.00	-4.39	-3.08	2.24	-1.82	0.28	-7.10	3.28	-11.54	3.71	tetranectin (plasminogen-binding protein); Tna	X79199	tetranectin precursor (n) (plasminogen-kringle 4 binding protein).	aka plasminogen binding protein -- a plasminogen-binding protein with a c-type lectin domain, is found in both serum and the extracellular matrix. it is a matricellular protein and plays a role in	9 71.0 cM	ECM (Matrix Prot)	
X83932	1.00	2.28	-3.02	1.55	-0.27	1.54	-1.90	0.20	-15.56	13.50	ryanodine receptor 1, skeletal muscle; Ryr1	X83932		provides a release mechanism for internal cellular ca2+, mutation associated with human malignant hyperthermia (mh)(omim 1456). ryr1 is predominant in skeletal muscle, but is also detectable in heart and in brain	7 10.0 cM	Receptor	
M91602	1.00	-1.04	-6.76	4.34	-1.48	0.21	-18.83	7.24	-16.81	3.83	myosin light chain, phosphorylatable, cardiac ventricles; Mylpc	M91602	myosin regulatory light chain 2, ventricular/cardiac muscle isoform (mlc-2)	a regulatory light chain predominantly expressed in ventricular cardiac muscle		Structural Protein	
Msa.1007.0	1.00	1.20	-10.87	7.61	-1.90	0.38	-26.29	5.63	-17.28	4.06	myosin light chain, phosphorylatable, cardiac ventricles; Mylpc	M91602	myosin regulatory light chain 2, ventricular/cardiac muscle isoform (mlc-2)	a regulatory light chain predominantly expressed in ventricular cardiac muscle		Structural Protein	
M29793	1.00	1.28	-6.52	3.56	-2.79	0.98	-19.87	14.88	-18.50	9.76	troponin C, cardiac/slow skeletal; Tncc	M29793	troponin c, slow skeletal and cardiac muscles (tn-c)	troponin is the central regulatory protein of striated muscle contraction. it consists of three components: tn-i which is the inhibitor of actomyosin apase, tn-t which contain the binding site for tropomyosin and tn-c. the binding of calcium	14 10.0 cM	Structural Protein	